

[illegible]

QY	1400	GGGGCACCACAGCAACCTGCAAGAAACCCGCCGAAATGCTGGGAGAGACACCGTGTACAG	1459
Db	483	GGGGCACCACAGCAACCTGCAAGAAACCCGCCGAAATGCTGGGAGAGACACCGTGTACAG	424
QY	1460	GAGCGGGTGTATGATGACGAGGTGAGGTGTGAAAGAGTCTCCGAGAAGGGGAGAGATCAT	1519
Db	423	GAGCGGGTGTATGATGACGAGGTGAGGTGTGAAAGAGTCTCCGAGAAGGGGAGAGATCAT	364
QY	1520	GTAAGCCCGGGAAGTAGGACCTGCTCCAGTGTGCTGGTGGTTGGCCGACCATGATCCCT	1579
Db	363	GTAAGCCCGGGAAGTAGGACCTGCTCCAGTGTGCTGGTGGTTGGCCGACCATGATCCCT	304
QY	1580	CCGAATCTGGTTGGGATCCAGCATACGCGCAATGTGCACAACAAATCAGCCCTGGCGAGAC	1639
Db	303	CCGAATCTGGTTGGGATCCAGCATACGCGCAATGTGCACAACAAATCAGCCCTGGCGAGAC	244
QY	1640	ACGAGCAGAGGAGAGACAGAGAAAGAAACACAGCATGGAACACAGTAATGAAT	1699
Db	243	ACGAGCAGAGGAGAGAGACAGAGAAAGAAACACAGCATGGAACACAGTAATGAAT	184
QY	1700	AAAACATATAATATTTAGCCCTGCTGTCTGTCTTACTGGCCAGGAATGGTACCAAT	1759
Db	183	AAAACATATAATATTTAGCCCTGCTGTCTGTCTTACTGGCCAGGAATGGTACCAAT	124
QY	1760	TTTTCAGTGTGGACTGACAGCTCTTTTGGCACAAGAGAGAAATTAACACTGTT	1819
Db	123	TTTTCAGTGTGGACTGACAGCTCTTTTGGCACAAGAGAGAAATTAACACTGTT	64
QY	1820	TCAAACCCGGGGAGTTGGCTGTGTAAAGAAACATTAAATGCTTTAGACAGTAA	1879
Db	63	TCAAACCCGGGGAGTTGGCTGTGTAAAGAAACATTAAATGCTTTAGACAGTAA	4
QY	1880	AAA 1882	
Db	3	AAA 1	
RESULT 10			
LOCUS	BO882838		
DEFINITION	BO882838	948 bp	EST 16-AUG-2002
ACCESSION	AGENCOURT_8627686	NIH_MGC_43	Homo sapiens
VERSION	5', mRNA sequence.		
KEYWORDS	BO882838		
SOURCE	BO882838.1	GI:22274846	
ORGANISM	human.		
REFERENCE	Homo sapiens		
AUTHORS	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
TITLE	Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.		
JOURNAL	1 (bases 1 to 948)		
COMMENT	NIH-MGC http://mhc.nci.nih.gov/ .		
	National Institutes of Health, Mammalian Gene Collection (MGC)		
	Unpublished (1999)		
	Contact: Robert Strausberg, Ph.D.		
	Email: cgabbs@email.nih.gov		
	Tissue Procurement: ATCC		
	CDNA Library Preparation: Rubin Laboratory		
	CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)		
	DNA Sequencing by: Agencourt Bioscience Corporation		
	Clone distribution: MGC clone distribution information can be		
	found through the I.M.A.G.E. Consortium/LNL at:		
	http://image.llnl.gov		
	Plate: LCM2492 row: k column: 01		
	High quality sequence stop: 533.		
FEATURES	Location/Qualifiers		
SOURCE	1. 948		
	/organism="Homo sapiens"		
	/db_xref="taxon:9606"		
	/clone="IMAGE:6291960"		
	/clone_lib="NIH_MGC_43"		
	/tissue_type="normal pigmented retinal epithelium"		
	/lab_host="Dh10B (phage-resistant)"		

Note: cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCAACGAG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-CDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies)

Note: this is a NIH-MGC Library. 1"

BASE COUNT	183 a	288 c	286 g	190 t	1 others
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JOURNAL
COMMENT

(CCAP/BICAP), Tumor Gene Index
Unpublished (1998)
Contact: Robert Strausberg, Ph.D.
Email: ccapbs-remail.nih.gov
Tissue Procurement: David N. Louis, M.D., Myrna R. Rosenfeld M.D.,
Ph.D.
cDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima
Bonaldi, Ph.D.
cDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone Distribution: NCI-CCAP clone distribution information can be

Query Match	29.1%	Score 352;	DB 14;	Length 948;
Best Local Similarity	100.0%	Pred. No. 0;		
Matches 552;	Conservative	0;	Mismatches	0;
			Indels	0;
				Gaps
QY	19	GCTGCTGGCCCGGAGACCCGAGCCGGAGAGACAGAGACCCGAGCCGGAGCCGAGG	78	
Db	8	GGTGTCTGGCCCCGGAGAGCCGAGACGGAGAGACAGAGACCCGAGCCGGAGCCGAGG	67	
QY	79	CGGGCGATTCAGAGCTCCGCGAGCCGGACACCTGCGGCTCTCTAAGCTACAGCGTGTCTC	138	
Db	68	CGGGCGATTCAGAGCTCCGCGAGCCGGACACCTGCGGCTCTCTAAGCTACAGCGTGTCTC	127	
QY	139	CGCGGAGAGAGGGCGGGGGCCCAAGACGCTCGGAGGACACAGCGCGTGCAGCCGGGCGAGC	198	
Db	128	CGGGAGAGAGAGGGCGGGGGCCCAAGACGCTCGGAGGACACAGCGCGTGCAGCCGGGCGAGC	187	
QY	199	CTCCGCTGCTGTGTCCTCTCTGATGCGCTTGCCCTCTCCCGGCCCGGGAGCTCCGGAG	258	
Db	188	CTCCGCTGCTGTGTCCTCTCTGATGCGCTTGCCCTCTCCCGGCCCGGGAGCTCCGGAG	247	
QY	259	AATGTGGGTCCTAAGGATCGGCGCACTTTTTCGGAATGTTTCTTCTTCCAGGCTTTGC	318	
Db	248	AATGTGGGTCCTAAGGATCGGCGCACTTTTTCGGAATGTTTCTTCTTCCAGGCTTTGC	307	
QY	319	GCTGCAATCCAGTGCTACCAAGTGTGAAGATTCCAGCTAACAAGACAGCTGCTCTCCCC	378	
Db	308	GCTGCAATCCAGTGCTACCAAGTGTGAAGATTCCAGCTAACAAGACAGCTGCTCTCCCC	367	
QY	379	CGAGTTCATGTGAATTTGACGCGTGAACGTTTCAAGACATGTGTGAGAAAGATGATGA	438	
Db	368	CGAGTTCATGTGAATTTGACGCGTGAACGTTTCAAGACATGTGTGAGAAAGATGATGA	427	
QY	439	GCAAAATGCCGGGATCATGTATCCGCAAGTCTGTGATATCAAGCGGCCGTTGTCATCGC	498	
Db	428	GCAAAATGCCGGGATCATGTATCCGCAAGTCTGTGATATCAAGCGGCCGTTGTCATCGC	487	
QY	499	CTTGTGCCGGGTACCAAGTCTTGTGCTCCCAAGGAAACTGAACCTCAATTTGCATCACTG	558	
Db	488	CTTGTGCCGGGTACCAAGTCTTGTGCTCCCAAGGAAACTGAACCTCAATTTGCATCACTG	547	
QY	559	CTGCAACACCCC 570		
Db	548	CTGCAACACCCC 559		

	FEATURES	source
	www.bioinformatics.org/bhrp/image/image.html Insert Length: 1143 Std Error: 0.00 Seq primer: -40bp from GlbD5 High quality sequence stop: 454. Location/Qualifiers	
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	/db.xref="taxon:9606"	
	/clone IMAGE:2467075"	
	/clone_lib="NCI-CCAP Brn25"	
	/tissue_type="anaplastic oligodendroglioma"	
	/lab_host="DH10B"	
	/note="Organ: brain; Vector: pRT73P-Pec (Pharmacia) with modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA was primed with a Not I - oligo(dT) primer (5' GTGTCACATCTGAAGTGAGACCGGCCCATAGGTGTTTTTTTTTTTTTTT T 3'); double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pRT73 vector. Library is normalized, and was constructed by Bento Soares and M.Felima Bonaldo."	
BASE COUNT	133 a 199 c 161 g 182 t 3 others	
ORIGIN		
Query Match	28.8%; Score 546; DB 9; Length 678;	
Best Local Similarity	99.8%; Pred. No. 0;	
Matches 596; Conservative	0; Mismatches 1; Indels 0; Gaps 0	
OY	1280 TGCAGAGACTGGCGCCGGGAGCCGGAAGACACAGCGCGCTGTGCACAAAGGGGGCGCGTC	1339
DB	597 TGCAGAGACTGGCGCCGGGAGCCGGAAGACACAGCGCGCTGTGCACAAAGGGGGCGCGTC	538
OY	1340 GGTGTGAGTAGTGGCAATGTACGCGCAGAGCGCTTCTGCTGTGGTGGCGTGTGCACAGCAC	1399
DB	537 GGGTGTGAGTAGTGGCAATGTACGCGCAGAGCGCTTCTGCTGTGGTGGCGTGTGCACAGCAC	478
OY	1400 GCCGACACACAGCACTTCGACGCAAAACC CGCCGCAAACTGTGTGGAGAGACAACCGTGTAC	1459
DB	477 GCCGACACACAGCACTTCGACGCAAAACC CGCCGCAAACTGTGTGGAGAGACAACCGTGTAC	418
OY	1460 GAGCGGGTTGATGACCGAGCTGAGGTAGAAAACGTCCTCCGAGAAGGGAGAGAGATCAT	1519
DB	417 GAGCGGGTTGATGACCGAGCTGAGGTAGAAAACGTCCTCCGAGAAGGGAGAGAGATCAT	358

RESULT 11	LOCUS	DEFINITION	ACCESSION	VERSION	KEYWORDS	SOURCE	ORGANISM	REFERENCE	AUTHORS	TITLE
AI936826/c	AI936826	678 bp mRNA	wp69n10.x1	NCI/CGAP_Brn25	Homo sapiens cDNA clone IMAGE:2467075.3 similar to SW:GP39_HUMAN O43194 PUTATIVE G PROTEIN-COUPLED RECEPTOR GP39.1, mRNA sequence.	AI936826	AI936826	GI:5675696	EST.	human.
							Homo sapiens			
							Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.			
							1 (bases 1 to 678)			
							NCI/NINDS-CGAP http://www.ncbi.nlm.nih.gov/ncicgap .			
							National Cancer Institute / National Institute of Neurological Disorders and Stroke, Brain Tumor Genome Anatomy Project			

OY	1220	GTAACCCCGGAGATACCACTTGGTTGGCCTGCAGCATGATCCT	298
Db	357	GTAGGCCCGGAAGTAGAACCCTGTCAGATCGTCTTG6GTTTGGCCCGACGATGATCCT	
OY	1580	CCGAAATCTGTTGGGCACTCCAGCATPACGGCCAAATGTACAACAATCAGCCCTGGGCAAC	1639
Db	297	CCGAATCTGTTGGGCACTCCAGCATPACGGCCAAATGTACAACAATCAGCCCTGGGCAAGAC	238
OY	1640	ACGAGCAGGAGGAGAGACAGAAAAAAAACACACAGCATGAGAACAACATAATGAAT	1699
Db	237	ACGAGCAGGAGGAGAGACAGAAAAAAAACACACAGCATGAGAACAACATAATGAAT	178
OY	1700	AAAACCATTAATATTATAGCCCCCTGTTCTGTACTGTGGCCAGGAAATGTACCAAT	1759
Db	177	AAAACCATTAATATTATAGCCCCCTGTTCTGTCTGTACTGTGGCCAGGAAATGTACCAAT	118
OY	1760	TTTTCAGTGTGACCTTGACAGCTTCTTTTCCACAAACAGAGAGAAATTTAACACTGTT	1819

Query Match	28.78;	Score 545;	DB 13;	Length 627;
Best Local Similarity	99.88;	Pred. No. 0;		

Ph.D.
CDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima
Bonafido, Ph.D.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CCRP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLN, send email to:
info@image.llnl.gov


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/organism="Homo sapiens"
/db.xref="taxon:9606"
/clone="IMAGE:3306972"
/clone_lib="NCI_CGAP_Brn23"
/tissue_type="gliblastoma (pooled)"
/lab_host="DH10B"
/note="Organ: brain; Vector: pT73D-Pac (Pharmacia) with a
modified polylinker. Site.1: Not I; Site.2: Eco RI; 1st
strand cDNA was primed with a Not I - oligo(dT) primer [5'
GTGTACCAATCTGAAGTGGAGGCGCCGACATATCTTTTCTTTTCTTTTCTTTT
T 3']; double-stranded cDNA was ligated to Eco RI
adaptors (Pharmacia), digested with Not I and Eco RI
into the Not I and Eco RI sites of the modified pT73 vector.
Library is normalized, and was constructed by Bento
Soares and M. Fatima Bonaldo."
BASE COUNT      110 a      161 c      128 g      152 t
ORIGIN

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Query Match      26.4%; Score 500; DB 12; Length 551;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 550; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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QY 1337 AGCGGGCGCTGTCGGTGGTGGATGCGCATGACGCGCGGCTTCGTTGGCGT 1386
|||||
DB 551 AGCGGGCGCTGTCGGTGGTGGATGCGCATGACGCGCGGCTTCGTTGGCGT 492
|||||
QY 1387 GCTGACGACAGCGGGGACGACACCTCTGACAAACCCCGGAAACCTGTCGAGG 1446
|||||
DB 491 GCTGACGACAGCGGGGACGACACCTCTGACAAACCCCGGAAACCTGTCGAGG 432
|||||
QY 1447 ACACGCTGACAGAGCGGGTGTGATGACCGAGCTAGTAAACACGCTCCGAGAAAG 1506
|||||
DB 431 ACACGCTGACAGAGCGGGTGTGATGACCGAGCTAGTAAACACGCTCCGAGAAAG 372
|||||
QY 1507 GGAGAGGATCATGTACGCGCGGAAAGTAGAGACCTGCTGCTGCTGGTTGGCCG 1566
|||||
DB 371 GGAGAGGATCATGTACGCGCGGAAAGTAGAGACCTGCTGCTGCTGGTTGGCCG 312
|||||
QY 1567 GAGCATGATGCTCGGAATCTGTTGGGATCAGCATGCGGCAATGTCACAAACATCA 1626
|||||
DB 311 GAGCATGATGCTCGGAATCTGTTGGGATCAGCATGCGGCAATGTCACAAACATCA 252
|||||
QY 1627 GCCCTGGGACAGACGAGGAGGAGAGACAGAAAAAGAAAAACAGCATGAGAAC 1686
|||||
DB 251 GCCCTGGGACAGACGAGGAGGAGAGACAGAAAAAGAAAAACAGCATGAGAAC 192
|||||
QY 1687 ACAGTAATGAATAAATCAATTAATATTAGCCCTCTGTTCTGCTTACTGGCCAG 1746
|||||
DB 191 ACAGTAATGAATAAATCAATTAATATTAGCCCTCTGTTCTGCTTACTGGCCAG 132
|||||
QY 1747 AATGTGATCAATTTTTCAGTGTGACCTTCTTTTGGCACAAGAGAGAGA 1806
|||||
DB 131 AATGTGATCAATTTTTCAGTGTGACCTTCTTTTGGCACAAGAGAGAGA 72
|||||
QY 1807 AATTAACACTGTTTCAAAACCGGGGAGTTGGCTGTGTTAAAGAAAGACATTAAATGCT 1866
|||||
DB 71 AATTAACACTGTTTCAAAACCGGGGAGTTGGCTGTGTTAAAGAAAGACATTAAATGCT 12
|||||
QY 1867 TTAGACAGTGT 1877
|||||
DB 11 TTAGACAGTGT 1

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RESULT 17
BIS54034      698 bp      mRNA      linear      EST_05-SRP-2001
LOCUS      603335426p1 NCI_CGAP_Brn67 Homo sapiens cDNA clone IMAGE:5309527
DEFINITION      5', mRNA sequence.
ACCESSION      BIS54034
VERSION      BIS54034.1 GI:15441348
KEYWORDS      EST.
SOURCE      human.
ORGANISM      Homo sapiens

```

```

REFERENCE
AUTHORS      NIH-MGC http://mgc.nci.nih.gov/.
TITLE      National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL
COMMENT      Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: rgs@bbs-rtm1.nih.gov
Tissue Procurement: David N. Louis, M.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at:
http://image.llnl.gov
Plate: LLM11784 row: d column: 08
High quality sequence stop: 687.

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FEATURES

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Location/Qualifiers
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/tissue_type="anaplastic oligodendroglioma with 1p/19q
loss"
/lab_host="DH10B (T1 phage-resistant)"
/note="Organ: brain; Vector: pCMV-SPORT6; Site.1: NotI;
Site.2: SalI; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 2.3 kb. Constructed by Life
Technologies. Note: this is a NCI_CGAP Library."

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BASE COUNT

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ORIGIN
131 a      231 c      204 g      132 t

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Query Match      26.3%; Score 498; DB 13; Length 698;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 618; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

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QY 19 GGTGTCGCGCCCGGAGCGCGAGCGGAGAGACAGAACCCGAGCGGGAGCGGAG 78
|||||
DB 17 GGTGTCGCGCCCGGAGCGCGAGCGGAGAGAGACAGAACCCGAGCGGGAGCGGAG 76
|||||
QY 79 CGGGCATCAGAGCTCCGCGAGCGGACCTGCGGCTCTCTAAGTACGACCGTCTCTC 138
|||||
DB 77 CGGGCATCAGAGCTCCGCGAGCGGACCTGCGGCTCTCTAAGTACGACCGTCTCTC 136
|||||
QY 139 CGGGCAGAGCGCGCGGCCCGACAGCTCGGAGCGACAGCGCTGACGCGGAGCGAGC 198
|||||
DB 137 CGGGCAGAGCGCGCGGCCCGACAGCTCGGAGCGACAGCGCTGACGCGGAGCGAGC 196
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QY 199 CTCGCGTCTGTCGCTCTCTCTGATGCGCTTGCCTCTCCGCGCCCGGGAGCTCGGGAG 258
|||||
DB 197 CTCGCGTCTGTCGCTCTCTCTGATGCGCTTGCCTCTCCGCGCCCGGGAGCTCGGGAG 256
|||||
QY 259 AATGTGGTCTTAGAGCATGCGGCACTTTTCCGATGTTCTTCTCCAGGCTTGG 318
|||||
DB 257 AATGTGGTCTTAGAGCATGCGGCACTTTTCCGATGTTCTTCTCCAGGCTTGG 316
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QY 319 GCTGCAATTCAGTGTACAGTGTGAAGAAATTCAGCTGAACAAAGACTGCTCTCC 378
|||||
DB 317 GCTGCAATTCAGTGTACAGTGTGAAGAAATTCAGCTGAACAAAGACTGCTCTCC 376
|||||
QY 379 CGAGTTCATTGTGAATTCAGCGGTGAAGCTTCAAGACATGTGTCAGAA- GAAGTATGG 437
|||||
DB 377 CGAGTTCATTGTGAATTCAGCGGTGAAGCTTCAAGACATGTGTCAGAA- GAAGTATGG 436
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QY 438 AGCAAGTCCCGGAGATCATGTAACGCAAGCTCTGATCATCATCAGGCGGCTGCTCATG 497
|||||
DB 437 AGCAAGTCCCGGAGATCATGTAACGCAAGCTCTGATCATCATCAGGCGGCTGCTCATG 496
|||||
QY 498 CCTCTCCGCGGTACAGATCTTCTGCTCCCAAGGAAACTGAACACTGATTGATCAGCT 557
|||||
DB 497 CCTCTCCGCGGTACAGATCTTCTGCTCCCAAGGAAACTGAACACTGATTGATCAGCT 556
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Qy	Dy	Dx	Qx
558	557	557	557
GCTGCAACACCCCTCTTGTGTAAAGGCCCAAGGCCCAAGAAAAGGGGAAGTTCTTGCCCTCG	GCTGCAACACCCCTCTTGTGTAAAGGCCCAAGGCCCAAGAAAAGGGGAAGTTCTTGCCCTCG	GCTGCAACACCCCTCTTGTGTAAAGGCCCAAGGCCCAAGAAAAGGGGAAGTTCTTGCCCTCG	GCTGCAACACCCCTCTTGTGTAAAGGCCCAAGGCCCAAGAAAAGGGGAAGTTCTTGCCCTCG
617	617	617	617
CCCTCAGGSCAAGGCGTCGC	CCCTCAGGSCAAGGCGTCGC	CCCTCAGGSCAAGGCGTCGC	CCCTCAGGSCAAGGCGTCGC
636	636	636	636
617	617	617	617
CCCTCAGGSCAAGGCGTCGC	CCCTCAGGSCAAGGCGTCGC	CCCTCAGGSCAAGGCGTCGC	CCCTCAGGSCAAGGCGTCGC
635	635	635	635

RESULT 18	
BF933693/c	
LOCUS	540 bp mRNA linear
DEFINITION	BF933693 nc80012.x1 NCI-CGAP-Brn23 Homo sapiens cDNA clone IMAGE:3440591 3'
EST 22-JAN-2001	

ACCESSION	BF9339693	GI:12357104
VERSION	BF9339693.1	
KEYWORDS	EST.	
SOURCE	human.	
ORGANISM	Homo sapiens	

REFERENCE	AUTHORS	TITLE
1 (bases 1 to 540)	Mammalia: Eutheria: Primates: Catarrhini; Homnidae; Homo.	
NCI/NINDS-CGAP	http://www.ncbi.nlm.nih.gov/ncicgap .	
National Cancer Institute	/ National Institute of Neurological	

JOURNAL COMMENT
Unpublished (1998)
Contact: Robert Strausberg, Ph.D.

Tissue Procurement: David N. Louis, Myrna R. Rosenfeld M.D.,
 Ph.D.
 cdna.Library.Preparation: M. Bento Soares, Ph.D., M. Fatima
 Bonaldo, Ph.D.
 cdna.Library.Arrayed by: Greg Lennon, Ph.D.
 DNA Sequencing by: Washington University Genome Sequencing Center
 Clone distribution: NCI-CCGAP clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL, send email to:
 info@image.llnl.gov
 Seq primer: -40Up from Glibco
 High quality sequence stop: 467.

FEATURES	Location/Qualifiers
source	1. .540

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/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:340591"
/clone_1lb="NCI CGAP_Brn23"
/tissue_type="glioblastoma (pooled)"
/lab_host="DHI0B"

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BASE COUNT
ORIGIN
108 a 158 c 124 g 150 t

Query Match	25.8%	Score	489	DB	12	Length	540
Best Local Similarity	99.8%	Pred. No.	0				
Matches	539	Conservative	0	Mismatches	1	Indels	0
						Gaps	0

1337 GTCCGTTGGAGTCCGCATGTACGCCAGCGCTTCTCCTGTTGGCGTCTGCACCGA 1390

540 GTCGGTGGTGGAGTCCGCATGTACGGCCAGCGCCTTCTCGTGGTTGGCGTGCTGCACCGA 481

139 / CAGGCGGCAGCAGCACCCTGCACGAACACCCGCCGAACCTGCTGCAGGACACCGTGA 1456

480 CAGGCGCAGCAGCACCTGGCACGAACACCCGCCGGAACCTGCTGGGAGGACACCGTGA 421

QY 1457 CAGGAGCGGCTTGATGACCGAGCTGAGCTAGAAAAACGCTCCGAGAAAGGGAGAGAGAT 1518
 |||||
 Db 420 CAGGAGCGGCTTGATGACCGAGCTGAGCTAGAAAAACGCTCCGAGAAAGGGAGAGAGAT 361

QY 1517 CATGTAGCGCCCGGAAGTAGGACCTCGTCCAGTGGTCTTGGGTTGGCCGACCATGAT 1576
|||||
Dd 360 CATGTAGCGCCCGGAAGTAGGACCTCGTCCAGTGGTCTTGGGTTGGCCGACCATGAT 301

QY 1577 CCTCCGAATCTGGTTGGGCAATCCAGCATACGCGCAATGTACACAAATCAGCCCTGGGCA 1638
|||||
Db 300 CCTCCGAATCTGGTTGGGCAATCCAGCATACGCGCAATGTACACAAATCAGCCCTGGGCA 241

QY 1637 GACACGAGCAGAGGAGGAGACACAGACAAAAACACGCGTCGAAACACAGTAAATG 1696
Db 240 GACACGAGCAGAGGAGGAGACACAGACAAAAACACGCGTCGAAACACAGTAAATG 181

DY 1697 AATAAACAATTAATTAGCCCTGTGTCGTACTGGCGCAGAATGTGCAC 1750
| | | | |
Db 180 AATAAAACAATAAATTTAGCCCTGTGTCGTACTGGCGCAGAATGTGCACC 121

Dy 1757 AATTTTCAGTGTGACCTTGACAGCTTCTTTGGCCAAAGCAAGAGNAATTTAACACT 1816
|||||
|||
Dd 120 AATTTTCAGTGTGACCTTGACAGCTTCTTTGGCCAAAGCAAGAGNAATTTAACACT 61

0Y 181/ GTTTCAACCCGGGGGAGTTGCGCTGTGTTAAAGAAAGACCATTAATGCTTTAGACAGTG 1876
 |||||
 Dd 60 GTTTCAACCCGGGGGAGTTGCGCTGTGTTAAAGAAAGACCATTAATGCTTTAGACAGTG 1

RESULT	19
A1742092/c	
LOCUS	
DEFINITION	
A1742092	578 bp mRNA linear EST 19-DEC-1999
wg38h03.x1	Soares_NSF_F8_9W_OT_PA_P.S1 Homo sapiens cDNA clone

IMAGE:236/413 3 similar to SM:GP39_HUMAN O43194 PUTATIVE G
PROTEIN-COUPLED RECEPTOR GPR39. , mRNA sequence.
AI142092
AI142092.1 GI:5110380
EST.
human.

ORGANISM	Homo sapiens
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
AUTHORS	1 (bases 1 to 578)
TITLE	NCI-CCAP http://www.ncbi.nlm.nih.gov/ncicgap .
JOURNAL	National Cancer Institute, Cancer Genome Anatomy Project (CCAP), Tumor Gene Index
COMMENT	Unpublished (1997)
CONTACT	Contact: Robert Strausberg, Ph.D.

Email: cgaps-remail.nih.gov
This clone is available royalty-free through LLNT ; contact the
IMAGE Consortium (info@image.lln.gov) for further information.
Insert Length: 806 Std Error: 0.00
Seq primer: -40up from Gabc
High quality sequence stop: 460.

FEATURES

source

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/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_1 IMAGE:2367413"
/clone_1db="Soares_NSF_F8_9W_OT_PA_P_S1"
/lab_host="DH10B"
/note="Organ: pooled: Vector: p77T3D-Pac (Pharmacia) with
a modified polylinker; Site_1: Not I; Site_2: Eco RI;
Equal amounts of plasmid DNA from five normalized
libraries were mixed, and ss circles were made in vitro.
Following HAP purification, this DNA was used as tracer in
a subtractive hybridization reaction. The driver was
PCR-amplified cDNAs from pools of 5,000 clones made from
the same 5 libraries. The pools consisted of the following
libraries and clonesIDs: Soares NBHSF pool 1:
3409384-3110919, 323208-125895 Soares Nb2HP pool 1:
145033-147335, 147720-148103, 146872-149255, 15002 -
150407, 151176-152327 Soares Nb2HF8-9W pool 1:

```


REFERENCE 1 (bases 1 to 527)
AUTHORS NCI-CCAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP) [Internet]. Bethesda, MD: National Cancer Institute; 2000. Available from: <http://www.ncbi.nlm.nih.gov/ncicgap/>

BASE COUNT	103 a	143 c	120 g	161 t
ORIGIN				

RESULT	22
B1913989	
LOCUS	
DEFINITION	B1913989 707 bp mRNA
ACCESSION	603180565651 NIH_MGC_121 Homo sapiens cDNA clone IMAGE:5244569 5', linear
VERSION	mRNA sequence.
KEYWORDS	B1913989
SOURCE	B1913989.1 GI:16178286
ORGANISM	EST.
REFERENCE	human.
AUTHORS	Homo sapiens
TITLE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
JOURNAL	Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
COMMENT	1 (bases 1 to 707)
	NIH-MGC http://mgc.ncl.nih.gov/.
	National Institutes of Health, Mammalian Gene Collection (MGC)
	Unpublished (1999)
	Contact: Robert Strausberg, Ph.D.

FEATURES	Location/Qualifiers
source	1. .707

Db	Accession	Source	Organism
Dn	459	TGATGTACCGCAAGTCCCTGTGCATCATCAGGGGCCCTGTCTCATGCCCCCTTCGGCCGGTGACC	518
Oy	513	AGTCCCTTCTGCTCCCCAGGAAACTGAATCAGTTTGTCATCAGCTGTGCAACACCCCTC	572
Dn	519	AGTCCCTTCTGCTCCCCAGGAAACTGAATCAGTTTGTCATCAGCTGTGCAACACCCCTC	578
Oy	573	TTTTGTACGGGCGCAAGGCCCAAGAAAAGGGAGAATTCTTGCTCGGCCCTCAGGCCA	628
Dn	579	TTTGTAACGGGCGCAAGGCCCAAGAAAAGGGAGAATTCTTGCTCGGCCCTCAGGCCA	634
RESULT	23		
LOCUS	Bf726459	530 bp	mRNA linear EST 05-JAN-2001
DEFINITION	bv06h03.y1 Human Lens cDNA (Un-normalized, unamplified): By Homo sapiens cDNA clone bv06h03 5', mRNA sequence.		
ACCESSION	Bf726459		
VERSION	Bf726459.1	GI:12042370	
KEYWORDS	EST.		
SOURCE	human.		
ORGANISM	Homo sapiens		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.		
AUTHORS	Mistow G.J., Bernstein,S., Behal,A. and Smith,D.		
JOURNAL	NEIBANK: EST analysis and bioinformatics for ocular genomics Invest. Ophthalmol. Vis. Sci. 41, (2000) In press		
COMMENT	Contact: Mistow G		

155 GCGCCAGAGCGCTGGGAGCCAGACCCGCTGACGCGGGGAGCCCTCCGCTGCTGCGC 214
 154 GCGCCAGAGCGCTGGGAGCCAGACCCGCTGACGCGGGGAGCCCTCCGCTGCTGCGC 213
 215 TCCCTGATGCGCTTGGCCCTCTCCGCGCGGGGAGCTCCGGGAGAGATGGGTCTTAGGC 274
 214 TCCCTGATGCGCTTGGCCCTCTCCGCGCGGGGAGCTCCGGGAGAGATGGGTCTTAGGC 273
 275 ATCCGCGCACTTTTGGGAGTTGTTCTTCCAGGCTTTGGCGCTCAATTCAGTGC 334
 274 ATCCGCGCACTTTTGGGAGTTGTTCTTCCAGGCTTTGGCGCTCAATTCAGTGC 333
 335 TACAGAGTGAAGAATTCACACTGACACAGACGCTCTCCCGGAGTATGTAAT 394
 334 TACAGAGTGAAGAATTCACACTGACACAGACGCTCTCCCGGAGTATGTAAT 393
 395 TGCAGGCTGAAGCTTCAAGATGTGTGAGAAAGATGATGAGCAAGTCCGGGATC 454
 394 TGCAGGCTGAAGCTTCAAGATGTGTGAGAAAGATGATGAGCAAGTCCGGGATC 453
 455 ATGACCGCAAGCTCTGTCATCAGCGGCTGTCTCATCGGCTTCCCGGGATCAG 514
 454 ATGACCGCAAGCTCTGTCATCAGCGGCTGTCTCATCGGCTTCCCGGGATCAG 513
 515 TCCCTGCTCCCGGAGAACTGACTCACTTTCATGCTGCTGCAACACCCCTTT 574
 514 TCCCTGCTCCCGGAGAACTGACTCACTTTCATGCTGCTGCAACACCCCTTT 573
 575 TGTAAAGGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 626
 574 TGTAAAGGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 625

RESULT 25
 LOCUS B0689033 879 bp mRNA linear EST 15-JUN-2002
 DEFINITION AGENCOURT_8063959 NIH_MGC_110 Homo sapiens cDNA clone IMAGE:6207625
 ACCESSION B0689033
 VERSION B0689033.1 GI:21814349
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 NIH-MGC http://mgc.nci.nih.gov/
 National Institutes of Health, Mammalian Gene Collection (MGC)
 Unpublished (1999)
 Contact: Robert Strausberg, Ph.D.
 Email: cgaops-remail.nih.gov
 Tissue Procurement: ATCC
 CDNA Library Preparation: Rubin Laboratory
 CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
 DNA Sequencing by: Agencourt Bioscience Corporation
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LNL at:
 http://image.lnl.gov
 Plate: LCM2364 row: a column: 02
 High quality sequence stop: 555.
 Location/Qualifiers
 1. 879
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="IMAGE:6207625"
 /clone_1ib="NIH_MGC_110"
 /tissue_type="ductal carcinoma, cell line"
 /lab_host="DH10B (phage-resistant)"
 /note="Organ: pancreas; Vector: pORF7; Site_1: XhoI;
 Site_2: EcoRI; cDNA made by oligo-dT priming.
 directionally cloned into EcoRI/XhoI sites using the
 following 5' adaptor: GGCACGAG(G). Library constructed by
 Ling Hong in the laboratory of Gerald M. Rubin (University

BASE COUNT 203 a 260 c 241 g 175 t
 ORIGIN
 Query Match 24.8%; Score 471; DB 14; Length 879;
 Best Local Similarity 99.8%; Pred. No. 0; Mismatches 1; Indels 0; Gaps 0;
 Matches 521; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 of California, Berkeley) using ZAP-cDNA synthesis kit
 (Stratagene) and Superscript II RT (Life Technologies).
 Note: this is a NIH-MGC Library."

871 TGACGAAATTTTCACTATGTAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 930
 22 TGACGAAATTTTCACTATGTAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 81
 931 CTGTATACCGAG 990
 82 CTGTATACCGAG 141
 991 GCATCGCTTTTGTAAAGCCCTCCAGTGTCCATTCATCCCTGATGGGGGATAGTTGA 1050
 142 GCATCGCTTTTGTAAAGCCCTCCAGTGTCCATTCATCCCTGATGGGGGATAGTTGA 201
 1051 GACTGACAGAGTGAAGTACGTTTCTTAAAGGAGAGAGAGAGAGAGAGAGAGAG 1110
 202 GACTGACAGAGTGAAGTACGTTTCTTAAAGGAGAGAGAGAGAGAGAGAGAGAG 261
 1111 CCGGCTTGACATCAACTCATGCTCTGTAAGAAACATTTCTCTGACAGAGAGAGAG 1170
 262 CCGGCTTGACATCAACTCATGCTCTGTAAGAAACATTTCTCTGACAGAGAGAGAG 321
 1171 GTTTCGCGCTGAGTTGGGCTCTAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 1230
 322 GTTTCGCGCTGAGTTGGGCTCTAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 381
 1231 GCTGCGCTGCTGTAAGAAAGTCTTAAAGAAATCTTCTGAGTCTCTTCCAGAGAG 1290
 382 GCTGCGCTGCTGTAAGAAAGTCTTAAAGAAATCTTCTGAGTCTCTTCCAGAGAG 441
 1291 GCGCGCGGAGCGGAG 1350
 442 GCGCGCGGAGCGGAG 501
 1351 GCGCATGTACGCGGAG 1392
 502 GCGCATGTACGCGGAG 543

RESULT 26
 LOCUS A1336858/c 515 bp mRNA linear EST 15-FEB-1999
 DEFINITION qx86g11.x1 NCI CGAP GC6 Homo sapiens cDNA clone IMAGE:2009444 3'
 ACCESSION A1336858
 VERSION A1336858.1 GI:4073785
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 NIH-MGC http://mgc.nci.nih.gov/
 National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
 Tumor Gene Index
 Unpublished (1997)
 Contact: Robert Strausberg, Ph.D.
 Email: cgaops-remail.nih.gov
 Tissue Procurement: Christopher A. Moskaluk, M.D., Ph.D., Michael
 R. Emmert-Buck, M.D., Ph.D.
 CDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima
 Bonaldo, Ph.D.
 CDNA Library Arrayed by: Greg Lennon, Ph.D.
 DNA Sequencing by: Washington University Genome Sequencing Center

	BE730800	1134 bp	mRNA	linear	EST 15-SEP-2000
LOCUS	BE730800				
DEFINITION	601570755T1 NIH_MGC_21 Homo sapiens CDNA clone IMAGE:3845557 5'				
ACCESSION	BE730800				
VERSION	BE730800.1	GI:10144792			
KEYWORDS	EST.				
SOURCE	human.				
ORGANISM	Homo sapiens				
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.				
REFERENCE	1 (bases 1 to 1134)				
AUTHORS	NIH-MGC http://mgc.ncl.nih.gov/.				
TITLE	National Institutes of Health, Mammalian Gene Collection (MGC)				
JOURNAL	Unpublished (1999)				
COMMENT	Contact: Robert Strausberg, Ph.D. Email: cgapbs@remail.nih.gov Tissue procurement: ATCC CDNA Library Preparation: Ling Hong/Rubin Laboratory CDNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNLN at: image.lnl.gov Plate: LNCm543 row: m column: 14 High quality sequence stop: 640.				
FEATURES	location/qualifiers				

FEATURES	SOURCE
location/Qualifiers	1. 1134
/organism="Homo sapiens"	/db_xref="taxon:9606"
/clone="IMAGE:3845557"	/clone_11b="NIH.MGC.21"
/tissue_type="Choriocarcinoma"	/lab_host="DH10B (phage-resistant)"
/note="Organ: placenta; Vector: pOT87; Site_1: XhoI; Site_2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAC(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies)."	329 a 320 c 308 a 127 f

BASE COUNT	329 a	320 c	308 g	177 t	ORIGIN
Query Match		22.5%	Score 426;	DB 12;	Length 1134;
Best Local Similarity		100.0%	Prod. No. 0;		
Matches 426; Conservative		0;	Mismatches	0;	Indels 0; Gaps 0;

QY	26	GGCCCCGGAGCGCCAGCGGCGAGAGCGACAGACCCCGACCGGGAGCCGAGCCGGCGGA	85
	1	GGCCCCGGAGCGCCAGCGGCGAGAGCGACAGACCCCGACCGGGAGCCGAGCCGGCGGA	60
QY	86	TGCAGGCTCCGCGAGCGGCGACCTCGGGCTCCCTCAACTACAGACCTGCTCTCCGGCGCA	145
Db	61	TGCAGGCTCCGCGAGCGGCGACCTCGGGCTCCCTCAACTACAGACCTGCTCTCCGGCGCA	120
QY	146	GCAACGCGGGGCCCGCAGCAGCCTCGGCACGCCACAGCCCGCTGCAGCGGGGAGCCTCGCCT	205
Db	121	GCAACGCGGGGCCCGCAGCAGCCTCGGCACGCCACAGCCCGCTGCAGCGGGGAGCCTCGCCT	180
QY	206	GCATGTCCCTCTCTGTATGGGCTTGCCCTCTCCGGCCCCGGGAGCTCGGGAGATGTGG	265
Db	181	GCATGTCCCTCTCTGTATGGGCTTGCCCTCTCCGGCCCCGGGAGCTCGGGAGATGTGG	240
QY	266	GTCTTAGGACATCGCGGCACACTTTTGTGGGAGATGTTCTTGCTCCAGGCTTTGGCCTCGAA	325
Db	241	GTCTTAGGACATCGCGGCACACTTTTGTGGGAGATGTTCTTGCTCCAGGCTTTGGCCTCGAA	300
QY	326	ATCCAGTGTCAACAGTGTGAAGATTCACAGTGAACAACACACTGCTCTCCCGAGATTC	385
Db	301	ATCCAGTGTCAACAGTGTGAAGATTCACAGTGAACAACACACTGCTCTCCCGAGATTC	360
QY	386	ATTGTGAATTGCACGCGGAACGTTTCAAGACATGTGTGAGAAAGACTGATGAGCAAAATG	445

Primer	Sequence	Position
D _b	ATTGGAATTCACGGTGAACGTTCAAGACATGTGTCAAGAAGAAGTGAACCAAGT	426
O _Y	GCCGGG	451
D _b	GCCGGG	426

RESULT	32				
A1150931/c					
LOCUS					
DEFINITION	A1150931	467 bp	mRNA	linear	EST 26-OCT-1994
	gb53c04.x1	NCI CGAP Brn23 Homo sapiens	CDNA clone	IMAGE:1703814	3'
	similar to	SN:NR1_FAT P20789	NEUROTENSIN RECEPTOR	TYPE 1	, mRNA
ACCESSION	A1150931				
VERSION	A1150931.1	GI:3679400			
KEYWORDS	EST.				
SOURCE	human.				
ORGANISM	Homo sapiens				

REFERENCE AUTHORS TITLE	JOURNAL COMMENT
Eukaryota: Metazoa: Chordata: Craniata: Vertebrata: Euteleostomi: Mammalia: Eutheria: Primates: Carnivorni: Homnidae: Homo. 1 (bases 1 to 467)	
NCI/NINDS-CGAP http://www.ncbi.nlm.nih.gov/ncicgap .	
National Cancer Institute / National Institute of Neurological Disorders and Stroke, Brain Tumor Genome Anatomy Project (CGAP/BRAP), Tumor Gene Index	
Unpublished (1998)	
Contact: Robert Strausberg Ph.D.	

Email: cgabos-remall.nih.gov
 Tissue Procurement: David N. Louis, M.D., Myrna R. Rosenfeld M.D.,
 Ph.D.
 cDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima
 Bonaldo, Ph.D.
 cDNA Library Arrayed by: Greg Lennon, Ph.D.
 DNA Sequencing by: Washington University Genome Sequencing Center
 clone distribution: MGI-CGAP clone distribution Information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bdnp/image/image.html
 Insert Length: 1149 Std Error: 0.00
 Seq primer: -40ml3 fwd. ET from Amersham
 High quality sequence stop: 425.

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FEATURES
SOURCE
Location/Qualifiers
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/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_image="IMAGE:1703814"
/clone_idb="NCI CGAP Brn23"
/tissue_type="glioblastoma (pooled)"
/lab_host="DH10b"
/note="Organ: brain; Vector: pT73D-Pac (Pharmacia) with a
modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st
strand cDNA was primed with a Not I - oligo(dT) primer [5'-
TGTATCCATATCTGACGTGGAGCGGCCGCACATATCTTTTTTTTTTTTTTTT
T3']"; double-stranded cDNA was ligated to Eco RI
adaptors (Pharmacia), digested with Not I and cloned into
the Not I and Eco RI sites of
the modified pT73 vector.
Library is normalized, and
Soares and M.Fatima Bonaldo."
BASE COUNT
106 a 119 c 92 g 150 t

```

Query Match	22.4%	Score 425;	DB 9;	Length 467;
Best Local Similarity	100.0%	Pred. No. 0;		
Matches 425;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
QY	1454	GTACAGAGGGGGTTGATGACCCGAGCTGAGGTACAAAAAGCTCTCCGAGGAAGGGAGAG	1513	
Db	467	GTACAGAGGGGGTTGATGACCCGAGCTGAGGTACAAAAAGCTCTCCGAGGAAGGGAGAG	408	
QY	1514	GATCATGTACGCCCGGAAGTAGAGACCTCGTCCAGTCTGCTTGGGTTTGGCCGAGGCAT	1573	
Db	407	GATCATGTACGCCCGGAAGTAGAGACCTCGTCCAGTCTGCTTGGGTTTGGCCGAGGCAT	348	

QY 1574 GATCTCCGAACTGTTGGGCAATCCAGATACGCCCAATGTCTACACAAATCAGCCCTGG 1633
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Db 347 GATCTCCGAACTGTTGGGCAATCCAGATACGCCCAATGTCTACACAAATCAGCCCTGG 288
QY 1634 GCACACACGACGAGGAGGAGAGACAGAGAAAGAAAACAGCATGAGAACAGTAA 1693
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Db 287 GCACACACGACGAGGAGGAGAGACAGAGAAAGAAAACAGCATGAGAACAGTAA 228
QY 1694 ATGATATAAACATATAATTTAGCCCCCTCTGTTCTGCTTACTGCGCAGGAATGGT 1753
Db 227 ATGATATAAACATATAATTTAGCCCCCTCTGTTCTGCTTACTGCGCAGGAATGGT 168
QY 1754 ACCAATTTTACGTTGAGCTTGACAGCTTTTGGCACAAGAGAAAGAAATTTTAC 1813
|||||
Db 167 ACCAATTTTACGTTGAGCTTGACAGCTTTTGGCACAAGAGAAAGAAATTTTAC 108
QY 1814 ACTGTTTCAACCCGGGAGGAGTGGCTGTGTTAAAGAAACATTAATGCTTAGACA 1873
Db 107 ACTGTTTCAACCCGGGAGGAGTGGCTGTGTTAAAGAAACATTAATGCTTAGACA 48
QY 1874 GTGTA 1878
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Db 47 GTGTA 43

RESULT 33
BE336607 480 bp mRNA linear EST 14-JUL-2000
LOCUS b68e04.y1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3030654 5', mRNA
DEFINITION BE336607
ACCESSION BE336607
VERSION BE336607.1 GI:9189000
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
TITLE NIH-MGC http://mgc.nci.nih.gov/.
JOURNAL National Institutes of Health, Mammalian Gene Collection (MGC)
COMMENT Unpublished (1999)
Other_ESTs: b68e04.x1
Contact: Robert Strausberg, Ph.D.
Email: cgaabs-remail.nih.gov
Tissue Procurement: DCM/DMP

CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
image.llnl.gov/image/html/resources.shtml
Seq primer: -40RP from Gibco
High quality sequence stop: 449.

FEATURES
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Location/Qualifiers
1..480

/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_image="3030654"
/clone_lib="NIH_MGC_9"
/tissue_type="adenocarcinoma cell line"
/lab_host="DH10B (phage-resistant)"
/note="Organ: ovary; Vector: pOTB7; Site_1: XhoI; Site_2:
ECORI; cDNA made by oligo-dt priming. Directionally
cloned into EcorI/XhoI sites using the following 5'
adaptor: GGCACGAG(G). Size-selected >500bp for average
insert size 1.8kb. Library constructed by Ling Hong in
the Laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies)."
BASE COUNT 86 a 154 c 153 g 87 t

Query Match

22.4%; Score 425; DB 10; Length 480;

Best Local Similarity 99.8%; Pred. No. 0;
Matches 475; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 GCACATCCGAGAGCTGTGTCGCGCCGAGAGCGGAGGAGAGACAGACCCG 60
|||||
Db 1 GCACATCCGAGAGCTGTGTCGCGCCGAGAGCGGAGGAGAGACAGACCCG 60
QY 61 CAGCCGGAGAGCCGAGCCGCGGCGATGACAGCTCCGAGGAGGACCTGGCTCTCTA 120
Db 61 CAGCCGGAGAGCCGAGCCGCGGCGATGACAGCTCCGAGGAGGACCTGGCTCTCTA 120
QY 121 AGCTACGACCGCTGCTCCGCGGAGAGCGGAGCGGCCAGCAGCCTGCGCAGCAGC 180
Db 121 AGCTACGACCGCTGCTCCGCGGAGAGCGGAGCGGCCAGCAGCCTGCGCAGCAGC 180
QY 181 CGCTGACGCGGAGAGCTCCGCTGCTGCTGCTCTGATGCGCTTGCCTCTCCG 240
Db 181 CGCTGACGCGGAGAGCTCCGCTGCTGCTGCTCTGATGCGCTTGCCTCTCCG 240
QY 241 GCGCGGAGAGCTCCGAGAGATGGGTCTCTAGCATGCGGAGCACTTTTGGGATGTT 300
Db 241 GCGCGGAGAGCTCCGAGAGATGGGTCTCTAGCATGCGGAGCACTTTTGGGATGTT 300
QY 301 CTTCCTCCAGGCTTTGGCTGCAATCCAGTCTACAGTGTGAAGATTCACCTGAA 360
Db 301 CTTCCTCCAGGCTTTGGCTGCAATCCAGTCTACAGTGTGAAGATTCACCTGAA 360
QY 361 CAGCAGCTGCTCTCCCGGAGTTGATGTAATGACAGGAGCACTTCAAGACATGTG 420
Db 361 CAGCAGCTGCTCTCCCGGAGTTGATGTAATGACAGGAGCACTTCAAGACATGTG 420
QY 421 TCAGAGAGAGTGTAGAGCAAGAGTCCGAGTATGTAACCGCAAGTCTGTGAT 476
Db 421 TCAGAGAGAGTGTAGAGCAAGAGTCCGAGTATGTAACCGCAAGTCTGTGAT 476

RESULT 34
BF126050 759 bp mRNA linear EST 24-OCT-2000
LOCUS 60176288Bp1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:4026092 5',
DEFINITION BF126050
ACCESSION BF126050
VERSION BF126050.1 GI:10965090
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
TITLE NIH-MGC http://mgc.nci.nih.gov/.
JOURNAL National Institutes of Health, Mammalian Gene Collection (MGC)
COMMENT Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgaabs-remail.nih.gov
Tissue Procurement: ATCC/DCTD/DTP
CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov
Plate: LCM855 row: o column: 21
High quality sequence stop: 723.

FEATURES
source
Location/Qualifiers
1..759

/organism="Homo sapiens"
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/clone_image="4026092"
/clone_lib="NIH_MGC_20"
/tissue_type="melanotic melanoma"
/lab_host="DH10B (phage-resistant)"
/note="Organ: skin; Vector: pOTB7; Site_1: XhoI; Site_2:
ECORI; cDNA made by oligo-dt priming. Directionally
cloned into EcorI/XhoI sites using the following 5'

adaptor: GGCACGAC(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies)."

BASE COUNT 191 a 192 c 221 g 155 t

ORIGIN

Query Match 22.4%; Score 424; DB 12; Length 759;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 424; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1186 TGGGCTCTAGTACTCGACGACATGATGATGAGCTGGGGCTGGGCTGCTCT 1245
|||||
Db 76 TGGGCTCTAGTACTCGACGACATGATGATGAGCTGGGGCTGGGCTGCTCT 135
|||||
QY 1246 GAAAGTGTCTTAAAGAAATCTTCTCACTTCTTCTGACAGAGACTGGGCGGAGCGGA 1305
|||||
Db 136 GAAAGTGTCTTAAAGAAATCTTCTCACTTCTTCTGACAGAGACTGGGCGGAGCGGA 195
|||||
QY 1306 AGAGCAACGGGCGCTGCACAAAGCGGCGCTGCTGCTGCTGAGTGGCATGACGGCA 1365
|||||
Db 196 AGAGCAACGGGCGCTGCACAAAGCGGCGCTGCTGCTGCTGAGTGGCATGACGGCA 255
|||||
QY 1366 GGGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1425
|||||
Db 256 GGGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 315
|||||
QY 1426 CCGCGCGAAACTGCTGCGAGGACACCGTGTACAGAGCGGGTGTATACGAGTGAAGT 1485
|||||
Db 316 CCGCGCGAAACTGCTGCGAGGACACCGTGTATACAGAGCGGGTGTATACGAGTGAAGT 375
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QY 1486 AGAAAAACGCTCTCCGAGAAAGGGAGAGATCATGTACGCCCGGAGTAGAGACTCTGTC 1545
|||||
Db 376 AGAAAAACGCTCTCCGAGAAAGGGAGAGATCATGTACGCCCGGAGTAGAGACTCTGTC 435
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QY 1546 AGTGTCTGCTGGGTTGGCGCGACCATGATCTCCGATCTGGTGGGATCCAGCATTA 1605
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Db 436 AGTGTCTGCTGGGTTGGCGCGACCATGATCTCCGATCTGGTGGGATCCAGCATTA 495
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QY 1606 CGCG 1609
|||||
Db 496 CGCG 499

RESULT 35
BF125134 843 bp mRNA linear EST 24-OCT-2000
LOCUS 601762356F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:4025340 5',
DEFINITION mRNA sequence.
ACCESSION BF125134
VERSION BF125134.1 GI:10964174
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 843)
NIH-MGC http://mgi.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC/DCTD/DRP
CDNA Library Preparation: Ling Hong/Rubin Laboratory
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov
Plate: LICM853 row: P column: 13
High quality sequence stop: 711.

FEATURES
source
I. 843
Location/Qualifiers

/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:4025340"
/clone_1ib="NIH_MGC_20"
/tissue_type="melanotic melanoma"
/lab_host="DHI08 (phage-resistant)"
/note="Organ: skin; Vector: pOTB7; Site: 1: XhoI; Site: 2:
EcoRI; cDNA made by oligo-dT priming. Directionally
cloned into EcoRI/XhoI sites using the following 5'
adaptor: GGCACGAC(G). Size-selected >500bp for average
insert size 1.8kb. Library constructed by Ling Hong in
the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies)."

BASE COUNT 225 a 192 c 255 g 171 t

ORIGIN

Query Match 22.4%; Score 424; DB 12; Length 843;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 424; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1186 TGGGCTCTAGTACTCGACGACATGATGATGAGCTGGGGCTGGGCTGCTCT 1245
|||||
Db 76 TGGGCTCTAGTACTCGACGACATGATGATGAGCTGGGGCTGGGCTGCTCT 135
|||||
QY 1246 GAAAGTGTCTTAAAGAAATCTTCTCACTTCTTCTGACAGAGACTGGGCGGAGCGGA 1305
|||||
Db 136 GAAAGTGTCTTAAAGAAATCTTCTCACTTCTTCTGACAGAGACTGGGCGGAGCGGA 195
|||||
QY 1306 AGAGCAACGGGCGCTGCACAAAGCGGCGCTGCTGCTGCTGAGTGGCATGACGGCA 1365
|||||
Db 196 AGAGCAACGGGCGCTGCACAAAGCGGCGCTGCTGCTGCTGAGTGGCATGACGGCA 255
|||||
QY 1366 GGGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1425
|||||
Db 256 GGGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 315
|||||
QY 1426 CCGCGCGAAACTGCTGCGAGGACACCGTGTACAGAGCGGGTGTATACGAGTGAAGT 1485
|||||
Db 316 CCGCGCGAAACTGCTGCGAGGACACCGTGTATACAGAGCGGGTGTATACGAGTGAAGT 375
|||||
QY 1486 AGAAAAACGCTCTCCGAGAAAGGGAGAGATCATGTACGCCCGGAGTAGAGACTCTGTC 1545
|||||
Db 376 AGAAAAACGCTCTCCGAGAAAGGGAGAGATCATGTACGCCCGGAGTAGAGACTCTGTC 435
|||||
QY 1546 AGTGTCTGCTGGGTTGGCGCGACCATGATCTCCGATCTGGTGGGATCCAGCATTA 1605
|||||
Db 436 AGTGTCTGCTGGGTTGGCGCGACCATGATCTCCGATCTGGTGGGATCCAGCATTA 495
|||||
QY 1606 CGCG 1609
|||||
Db 496 CGCG 499

RESULT 36
BM709964 571 bp mRNA linear EST 28-FEB-2002
LOCUS BM709964
DEFINITION UI-E-COI-agg-c-21-0-UI.r1 UI-E-COI Homo sapiens cDNA clone
ACCESSION BM709964
VERSION BM709964.1 GI:19023222
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 571)
Bonaldo, M.F., Lennon, G. and Soares, M.B.
Normalization and subtraction: two approaches to facilitate gene
discovery
JOURNAL Genome Res. 6 (9), 791-806 (1996)
MEDLINE 9704477
COMMENT Contact: Soares, MB

REFERENCE 1 (bases 1 to 571)
AUTHORS Bonaldo, M.F., Lennon, G. and Soares, M.B.
TITLE Normalization and subtraction: two approaches to facilitate gene
discovery
JOURNAL Genome Res. 6 (9), 791-806 (1996)
MEDLINE 9704477
COMMENT Contact: Soares, MB

Program for Rat Gene Discovery and Mapping

University of Iowa
451 Eckstein Medical Research Building Iowa City, IA 52242, USA
Tel: 319 335 8250
Fax: 319 335 9565

Email: mscares@blue.weeg.uiowa.edu
mscares@blue.uiowa.edu

Tissue Procurement: Dr. Gregg Hageman

CDNA Library Preparation: Dr. M. Bento Soares, University of Iowa

CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa

CDNA Sequencing by: Dr. M. Bento Soares, University of Iowa

CDNA Distribution: Researchers may obtain clones from Research Genetics (www.resgen.com).

Seq primer: M13 Reverse.

FEATURES

SOURCE

Location/Qualifiers

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1..571
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="UI-E-COI-agg-c-21-0-UI"
/clone_lib="UI-E-COI"
/tissue_type="optic nerve"
/dev_stage="adult"
/lab_host="DH10B (Life Technologies) (T1 phage resistant)"
/note="Organ: eye; Vector: pT73-Pac (Pharmacia) with a modified polylinker; Site.1: EcoR I; Site.2: Not I; UI-E-COI is a normalized cDNA library containing the following tissue(s): optic nerve. The library was constructed according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. First strand cDNA synthesis was primed with an oligo-dT primer containing a Not I site. Double stranded cDNA was ligated to an EcoR I adaptor, digested with Not I, and cloned directionally into pT73-Pac vector. The oligonucleotide used to prime the synthesis of first-strand cDNA contains a library tag sequence that is located between the Not I site and the (dT)18 tail. The sequence tag for this library is CCATTAGTG. This library was created for the program, Gene Discovery in the Visual System, supported by National Eye Institute (NEI)."
```

BASE COUNT 100 a 189 c 170 g 109 t 3 others

ORIGIN

Query Match 22.3%; Score 423; DB 14; Length 571;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 423; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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19 GGTGCTGCGCCGGAGCGCGAGGAGACAGACCCGCGGAGCCGAGCG 78
15 GGTGCTGCGCCGGAGCGCGAGGAGACAGACCCGCGGAGCCGAGCG 74
79 CGGCGGAGGAGGCTCCGCGAGCGGACCTGCTCTTAAGCTACGACCGTCTC 138
75 CGGCGGAGGAGGCTCCGCGAGCGGACCTGCTCTTAAGCTACGACCGTCTC 134
139 CGGCGGAGGAGGCGGCGCGCGAGCGGACCTGCGGACCGCGGCGGCGGCG 198
135 CGGCGGAGGAGGCGGCGCGCGAGCGGACCTGCGGACCGCGGCGGCGGCG 194
199 CTGCGGAGGAGGCGGCGGCGGAGCGGACCTGCGGACCGCGGAGCGGAG 258
195 CTGCGGAGGAGGCGGCGGCGGAGCGGACCTGCGGACCGCGGAGCGGAG 254
259 AATGAGGAGGAGGCGGCGGAGCGGACCTGCGGAGGAGGAGGAGGAGGAG 318
255 AATGAGGAGGAGGCGGCGGAGCGGACCTGCGGAGGAGGAGGAGGAGGAG 314
319 GGTGCAAAATCCAGTGTACAGTGTGAAGAATTCACGTCGACGAGTCTCTCC 378
315 GGTGCAAAATCCAGTGTACAGTGTGAAGAATTCACGTCGACGAGTCTCTCC 374
379 CGAGTTTCATTGTAATGACAGGTGAAGCTTCAAGACATGTGTGCAAGAAAGTATGA 438
375 CGAGTTTCATTGTAATGACAGGTGAAGCTTCAAGACATGTGTGCAAGAAAGTATGA 434
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OY 439 GCA 441
DB 435 GCA 437

RESULT 37

A1018769/c

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

FEATURES

SOURCE

1..537
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:1639038"
/clone_lib="Soares_testis_NHT"
/sex="male"
/lab_host="DH10B"
/note="Vector: pT73D-Pac (Pharmacia) with a modified polylinker; Site.1: Not I; Site.2: Eco RI; 1st strand cDNA was prepared from mRNA obtained from Clontech Laboratories Inc. and primed with a Not I - oligo(dT) primer [5' TGTTCAATCTGAAGTGTGAGCGGCGGCGGACCAATTTTTTTTTTTT 3']. Double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT73 vector. Library went through one round of normalization to Cot5, and was constructed by Bento Soares and M. Fatima Bonaldo."

BASE COUNT 105 a 147 c 126 g 159 t

ORIGIN

Query Match 21.9%; Score 415; DB 9; Length 537;
Best Local Similarity 99.6%; Pred. No. 0;
Matches 515; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

```
1354 CATGTACGCGGAGCGGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1413
537 CATGTACGCGGAGCGGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 478
1414 CCGTACGAGAACCGCGGCAAACTGTGCGAGACACGCTGTACAGAGAGGGTTGATGA 1473
477 CCGTACGAGAACCGCGGCAAACTGTGCGAGACACGCTGTACAGAGAGGGTTGATGA 418
1474 CCGAGCTGAGGTAGAAAACGCTCTCGAGAGGAGGAGGAGATCATGTACGCGGAGAGT 1533
417 CCGAGCTGAGGTAGAAAACGCTCTCGAGAGGAGGAGGAGATCATGTACGCGGAGAGT 358
1534 AGGACCTGCTCAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1593
```

Db	357	AGGACCTCGTCCAGTCTGCTGGGTTTTGGCCGAGCCATGATTCCTCCGAATCTGGTTGG	298
QY	1594	GCATCCAGCATACGGCCCAATGTGCACAACATATAGCCCTTGCGCAGACAGCAGAGAGGGA	1653
Db	297	GCATCCAGCATACGGCCCAATGTGCACAACATATAGCCCTTGCGCAGACAGCAGAGAGGGA	238
QY	1654	GAGACAGAGAAAGAAAAACACAGCATGAGAACACAGTAATGAATAAACCATAAATA	1713
Db	237	GAGACAGAGAAAGAAAAACACAGCATGAGAACACAGTAATGAATAAACCATAAATA	178
QY	1714	TTTAGCCCCCTGTTCTGTGCTTTACTTGCGCCAGAAATGTTACATTTTTCAGTGTGGA	1773
Db	177	TTTAGCCCCCTGTTCTGTGCTTTACTTGCGCCAGAAATGTTACATTTTTCAGTGTGGA	118
QY	1774	CTTGACAGCTCTTTTGGCCACAAGCAAGAGAAATTTAACTGTTTCAACCCGGGGGA	1833
Db	117	CTTGACAGCTCTTTTGGCCACAAGCAAGAGAAATTTAACTGTTTCAACCCGGGGGA	58
QY	1834	GTTGCTGTGTTAAAGAAAGACATTTAATGCTTTAG	1870
Db	57	GTTGCTGTGTTAAAGAAAGACATTTAATGCTTTAG	21

RESULT	38				
LOCUS	B1544761				
DEFINITION	B1544761	688 bp	mRNA	linear	EST 05-SEP-2001
ACCSSION	60922402	seq1	NIH_MGC_95	Homo sapiens	CDNA clone IMAGE:5284638 5',
VERSION	B1544761				
KEYWORDS	B1544761.1	GI:15432073			
SOURCE	Est.				
	human.				

REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

Mammalia; Euthetia; Primates; Catarrhini; Hominoidea; Homo.
1 (bases 1 to 688)
NIH-MGC <http://mgc.ncl.nih.gov/>.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.

```

FEATURES
source
      tissue Procurement: Miklos Palcovits, M.D., Ph.D.
      cDNA Library Preparation: Michael J. Brownstein (NHGRI), Shiroki
      Toshiyuki and Piero Carninci (RIKEN)
      cDNA library Arrayed by: The I.M.A.G.E. Consortium (LNL)
      DNA Sequencing by: Incyte Genomics, Inc.
      Clone distribution: MGC clone distribution information can be
      found through the I.M.A.G.E. Consortium/LNL at:
      http://image.jnl.gov
      Plate: L14M1719 row: 9 column: 07
      High quality sequence stop: 688.
      Location/Qualifiers
      I..688

```

```

/notes-Organ: brain; Vector: pBluescriptsp (modified
pBluescript KS+); Site-1: BamHI; Site-2: SalI-XhoI (9ctag
); Oligo-dT primed using primer 5'-TTTTTTTTTTTTTTTTVNN-3',
size-selected for average insert size 2.5 kb and
normalized to ROT 5. This is a primary library enriched
for full-length clones and constructed using the
Cap-trapper method (Carninci, in preparation). Library
constructed by M. Brownstein (NIMH/NHGRI, National
Institutes of Health). Note: this is a NIH_MGC Library."

```

Query Match 21.5%; Score 408; DB 13; Length 688;

	Best Local Similarity	100.0%	Pred. No. 0:
Matches	408:	Conservative	0: Mismatches 0: Indels 0: Gaps 0:
QY	19	GGTGTCCGGCCGGGAGCGCGAGCGGGAGAGACAGACC	CGGAGCCGGAGCCCGACG 78
Db	194	GGTGTCTGGCCCCGGGAGCGCGAGCGGGAGAGACAGACC	CGGAGCCGGAGCCCGACG 253
QY	79	CGGGGATGCAAGGCTCCGGAGCGGGACCTCGGTCTCTTAAGT	ACGACCCTGCTTC 138
Db	254	CGGGGATGCAAGGCTCCGGAGCGGGACCTCGGTCTCTTAAGT	ACGACCCTGCTTC 313
QY	139	CGCGGCACAGCGCGGGGCCACAGACCTTCGGACACACACCG	CGGTGCAGCCGGGGACG 198
Db	314	CGCGGCACAGCGGGGCCACAGACCTTCGGACACACACCG	CGGTGCAGCCGGGGACG 373
QY	139	CTCCGCTCTGTGCGCTTCCTTGATGCGCTTGCCTCCGGCC	CGGGACCTCCGGAG 258
Db	374	CTCCGCTCTGTGCGCTTCCTTGATGCGCTTGCCTCCGGCC	CGGGACCTCCGGAG 433
QY	259	AATGGGGTCCCTAAGGCATCGGGCAACTTTTGGGAGATTG	TTCTTTCCTCCAGCCTTTGC 318
Db	434	AATGGGGTCCCTAAGGCATCGGGCAACTTTTGGGAGATTG	TTCTTTCCTCCAGCCTTTGC 493
QY	319	GCTGCAATTCACAGTCTCCACAGTGGAGAAATTCACAGT	GTGAACAACGACTCTCTCC 378
Db	434	GCTGCAATTCACAGTCTCCACAGTGGAGAAATTCACAGT	GTGAACAACGACTCTCTCC 553
QY	379	CGAGTTCAATTGTGAATTGCACGGGTGAACGTTCAAGAC	TATGTTCAGAA 426
Db	554	CGAGTTCAATTGTGAATTGCACGGGTGAACGTTCAAGAC	TATGTTCAGAA 601

RESULT	39
B1669845	
LOCUS	690 bp
DEFINITION	mRNA linear
	603293444.F1 NIH_MGC_96 Homo sapiens cDNA clone IMAGE:5312889 5' ,
ACCESSION	B1669845
VERSION	B1669845
KEYWORDS	EST.
SOURCE	human.
ORGANISM	Homo sapiens

REFERENCE	AUTHORS	TITLE	JOURNAL	COMMENT
1 (bases 1 to 690)	NTI-MGC	http://mgc.ncl.nih.gov/	National Institutes of Health, Mammalian Gene Collection (MGC)	Unpublished (1999)
	Contact:	Robert Strausberg, Ph.D.		

tissue Procurement: Miklos Palkovits, M.D., Ph.D.
 cDNA Library Preparation: Michael J. Brownstein (NHGRI), Shiraiki
 Toshiyuki and Piero Carninci (RIKEN)
 cDNA library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
 Plate: LLAM1792 row: p column: 10
 High quality sequence stop: 690.
 Location/Qualifiers
 1..690

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/note="Organ: brain; Vector: pBluescript (modified
pBluescript KS+); Site_1: BamHI; Site_2: SalI-XhoI (gtcag
); Oligo-dT primed using primer 5'-TTTTTTTTTTTTTTTTTN-3',
size-selected for average insert size 2.3 kb and
normalized to ROT 5. This is a primary library enriched

```


similar to SW:NTR_RAT P20789 NEUROTENSIN RECEPTOR ;, mRNA sequence.
 AA613995
 VERSION AA613995.1 GI:2466129
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE 1 (bases 1 to 396)
 AUTORS NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
 TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
 Tumor Gene Index
 JOURNAL Unpublished (1997)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgaps-remail.nih.gov
 Tissue Procurement: L. Jeffrey Medeiros, M.D., Michael R.
 Emmert-Buck, M.D., Ph.D.
 CDNA Library Preparation: Stratagene, Inc., David B. Krizman,
 Ph.D.
 CDNA Library Arraying: Greg Lennon, Ph.D.
 DNA Sequencing by: Washington University Genome Sequencing Center
 Clone distribution: NCI-CGAP clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bdrip/image/image.html
 Seq primer: -40m13 fwd. RT from Amersham
 High quality sequence stop: 395.
 Location/Qualifiers
 1..396
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="IMAGE:1113710"
 /clone_lib="NCI-CGAP-AA1"
 /tissue_type="adrenal adenoma"
 /note="Organ: adrenal gland; Vector: Bluescript SK-;
 Site:1: EcoRI; Site:2: XhoI; Cloned unidirectionally.
 Primer: Oligo dt. Two pooled bulk adrenal adenomas. 5'
 adaptor sequence: 5' GAATTCGGACACAG 3' 3' adaptor
 sequence: 5' CTCGAGTCTTTTCTTTTCTTTT 3' Average insert
 size: 1.6 kb."
 BASE COUNT 56 a 135 c 103 g 102 t
 ORIGIN
 Query Match 20.9%; Score 396; DB 9; Length 396;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 396; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1296 CGGAGCGCAAGAGCAACGGCGCTGCACAAACGGCGCTGTCGGTGGAGTGGCGCA 1355
 |||||||
 DB 396 CGGAGCGCAAGAGCAACGGCGCTGCACAAACGGCGCTGTCGGTGGAGTGGCGCA 337
 QY 1356 TGTACGCGCAGGCGCTTCTGCTGGTGGCTGTCAGCAGAGCGCGCAGCAGCACC 1415
 |||||||
 DB 336 TGTACGCGCAGGCGCTTCTGCTGGTGGCTGTCAGCAGAGCGCGCAGCAGCACC 277
 QY 1416 TGTACGCAACACCGCGCAAACTCTCGAGAGCAACCGTGTACAGAGAGCGGTTGATGACC 1475
 |||||||
 DB 276 TGTACGCAACACCGCGCAAACTCTCGAGAGCAACCGTGTACAGAGAGCGGTTGATGACC 217
 QY 1476 GAGCTGAGGTAGAAAAAGCTCTCGAGAGAGGAGGAGTCTATGACGCCCGGAAGTAG 1535
 |||||||
 DB 216 GAGCTGAGGTAGAAAAAGCTCTCGAGAGAGGAGGAGTCTATGACGCCCGGAAGTAG 157
 QY 1536 GACCTGTCCAGTCTGCTGGTGGTGGCGCAGCATGATCTCTCCGAATCTGTTGGG 1595
 |||||||
 DB 156 GACCTGTCCAGTCTGCTGGTGGTGGCGCAGCATGATCTCTCCGAATCTGTTGGG 97
 QY 1596 ATCCAGCATAGCGCAATCTCAACAATCAGCCCTGGGCAAGCAGAGAGAGAGAGA 1655
 |||||||
 DB 96 ATCCAGCATAGCGCCATCTCAACAATCAGCCCTGGGCAAGCAGAGAGAGAGAGA 37
 QY 1656 GACAGAGAAAAAGAAACACAGCATGAGAACAGT 1691
 |||||||

DB 36 GACAGAGAAAAAGAAACACAGCATGAGAACACAGT 1
 RESULT 42
 A1391683/c
 LOCUS
 DEFINITION 452 bp mRNA linear EST 17-MAR-1999
 qy93f04.x1 NCI-CGAP Brn25 Homo sapiens CDNA clone IMAGE:2019583 3'
 similar to SW:NTR_RAT P20789 NEUROTENSIN RECEPTOR TYPE 1 ;, mRNA
 sequence.
 ACCESION A1391683
 VERSION A1391683.1 GI:4217687
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE 1 (bases 1 to 452)
 AUTORS NCI/NINDS-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
 TITLE National Cancer Institute / National Institute of Neurological
 Disorders and Stroke, Brain Tumor Genome Anatomy Project
 (CGAP/BRGAP), Tumor Gene Index
 JOURNAL Unpublished (1998)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgaps-remail.nih.gov
 Tissue Procurement: David N. Louis, M.D., Myrna R. Rosenfeld M.D.,
 Ph.D.
 CDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima
 Bonaldo, Ph.D.
 CDNA Library Arrayed by: Greg Lennon, Ph.D.
 DNA Sequencing by: Washington University Genome Sequencing Center
 Clone distribution: NCI-CGAP clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bdrip/image/image.html
 Insert length: 1183 Std Error: 0.00
 Seq primer: -40UP from Gibco
 High quality sequence stop: 451.
 Location/Qualifiers
 1..452
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 /db_xref="taxon:9606"
 /clone="IMAGE:2019583"
 /clone_lib="NCI-CGAP-Brn25"
 /tissue_type="anaplastic oligodendroglioma"
 /lab_host="DH10B"
 /note="Organ: brain; Vector: pT73D-Pac (Pharmacia) with a
 modified polylinker; Site:1: Not I; Site:2: Eco RI; 1st
 strand cDNA was primed with a Not I - oligo(dT) primer (5'
 TGTACCAATCTGAGAGGAGGAGGCGCGCATAGTCTTTTCTTTTCTTTT
 T 3'); double-stranded cDNA was ligated to Eco RI
 adaptors (Pharmacia), digested with Not I and cloned into
 the Not I and Eco RI sites of the modified pT73 vector.
 Library is normalized, and was constructed by Bento
 Soares and M.Fatima Bonaldo."
 BASE COUNT 94 a 122 c 99 g 137 t
 ORIGIN
 Query Match 20.8%; Score 394; DB 9; Length 452;
 Best Local Similarity 99.8%; Pred. No. 0;
 Matches 444; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1433 AAATGCTGCGAGAGACCGCTGTACAGAGCGGTTGATGACCGAGTGGTAGAAAA 1492
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 DB 445 AAATGCTGCGAGAGACCGCTGTACAGAGCGGTTGATGACCGAGTGGTAGAAAA 386
 QY 1493 CGTCTCCGAGAGAGGAGAGATCATGTACGCCCGGAAGTAGACCTCGCAGTGTG 1552
 |||||||
 DB 385 CGTCTCCGAGAGAGGAGAGATCATGTACGCCCGGAAGTAGACCTCGCAGTGTG 326
 QY 1553 CTGGGTTGGCGGAGCGCATGTATCTCCGAATCTGTTGGCATCAGCATAGGCCAA 1612
 |||||||
 DB 325 CTGGGTTGGCGGAGCGCATGTATCTCCGAATCTGTTGGCATCAGCATAGGCCAA 266
 QY 1613 TGTACAAACATCAGCCCTGGGCAAGCAGAGAGAGAGAGAGAGAGAGAGAAAA 1672

Db	265	TGTCACAAACATTCAGCCCTGGCGACAGCACGAGCGAGGGGAGAGACAGACAAAGAAATAAAA	206
Qy	1673	CACAGCAGTACAGACACAGTAAATGAATTAACCAATPAAATAATTTAGACCCCTGTCTGTCTGT	1732
Db	205	CACAGCATGACACACAGTAAATGAATTAACCAATPAAATAATTTAGACCCCTGTCTGTCTGT	146
Qy	1733	GCTTACTGCGCCAGGAAATGTGTACCAATTTTTCAGTGTGTGACCTTGACAGCTTTCTTTTGCC	1792
Db	145	GCTTACTGCGCCAGGAAATGTGTACCAATTTTTCAGTGTGTGACCTTGACAGCTTTCTTTTGCC	86
Qy	1793	ACAACGAGAGAGATTTAACTGTTCACAAACCCGGGGAGTGGCTGTGTAAAGAAA	1852
Db	85	ACAACGAGAGAGATTTAACTGTTCACAAACCCGGGGAGTGGCTGTGTAAAGAAA	26
Qy	1853	GACCATTAATGCTTTAGACAGTGT	1877
Db	25	GACCATTAATGCTTTAGACAGTGT 1	

RESULT	43
A1499630/c	
LOCUS	
DEFINITION	396 bp mRNA linear EST 12-MAY-1999
A1499630	
tcoo3bot.x1	NCI_CGAP_Ut2 Homo sapiens cDNA clone IMAGE:217941 3'
similar to	SM:NMR1_RAT P20789 NEUROTENSIN RECEPTOR TYPE 1 ; mRNA sequence.

ACCESSION	A1499630	GI:4391612
VERSION	A1499630.1	
KEYWORDS	EST.	
SOURCE	human.	
ORGANISM	Homo sapiens	

REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

Eukaryota; Euteleostomi; Chordata; Ctenidi; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
1 (bases 1 to 396)
NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.

Email: cgapbs-remail.nih.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R. Emmert-Buck, M.D., Ph.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: www.bio.llnl.gov/bdip/image/image.html
Insert Length: 826 Std Error: 0.00
Seq primer: -40UP from Gibco
High quality sequence stop: 395
POLYA-No.

FEATURES	Location/Qualifiers
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	/organism="Homo sapiens"
	/db_xref="taxon:9606"
	/clone="IMAGE:2177941"
	/clone_1ib="NCI CGAP_Ut2"
	/tissue_type="moderately-differentiated endometrial adenocarcinoma, 3 pooled tumors"
	/lab_host="DH10B"
	/note="Organ: uterus; Vector: pCMV-SPORT6; Site_1: Salt; Site_2: NotI; Cloned unidirectionally. Primer: Oligo dt. Average insert size 1.85 kb. Life Technologies catalog #: 11539-012"
BASE COUNT	62 a 124 c 96 g 114 t
ORIGIN	

Query Match	20.6%	Score 390;	DB 9;	Length 396.
Best Local Similarity	100.0%	Pred. No. 0;		
Matches 330;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0

QY 1328 GCGGGCGCTGTCGCTGCTGAGTGGGCATGTACGGCAGCGCGCTTCTCGTGGTTGCGTGC 1387

Db	396	GGGGGGCGTGGTGGTGGATGGATGGCATGTACCGGAGGGGCTTCTCTGGTTGGCCG	337
QY	1388	CTGCACGCGACAGCGGCGAGCAGCAGCACTTGCACGACACCGCGGAATCTGTCGAGGA	1447
Db	336	CTGCACGCGACAGCGGCGAGCAGCAGCACTTGCACGACACCGCGGAATCTGTCGAGGA	277
QY	1448	CACCGGTACAGGAGCGGGTTATATACCAGACTAGGTAAAGAAAAAGTCTCGAGAAAGG	1507
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RESULT 44	
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LOCUS	654 bp mRNA linear EST 15-SEP-2000
DEFINITION	601580186F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3928868 5', mRNA sequence.
ACCESSION	BE746601
VERSION	BE746601.1 GI:10160593
KEYWORDS	EST.
SOURCE	human.

ORGANISM *Homo sapiens*
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE
NIH-MGC <http://mgc.ncl.nih.gov/>.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.

Email: cgabds-remail@nih.gov
Tissue Procurement: DCTD/DTF
cDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MCC clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at: image.llnl.gov
Plate: LNCM60 row: 1 column: 21
High quality sequence stop: 651.

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Location/Qualifiers
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/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_image="3928868"
/clone_lib="NH_MJC_9"
/tissue_type="adenocarcinoma cell line"
/lab_host="DH10B (phage-resistant)"
/note="Organ: ovary; Vector: pOTB7; Site:1: XhoI; Site:2:
EcoRI; cDNA made by oligo-dT priming. Directionally
cloned into EcoRI/XhoI sites using the following 5'
adaptor: GCCACGAG(5). Size-selected >500bp for average
insert size 1.8kb. Library constructed by Ling Hong in
the laboratory of Gerald M. Rubin (University of

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BASE COUNT	ORIGIN
121 a	219 c
	187 g
	126 t
	1 others

115

GenCore version 5.1.3
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OM nucleic - nucleic search, using sw model

Run on: November 7, 2002, 09:53:42 ; Search time 71.0849 Seconds
(without alignments)
8184.096 Million cell updates/sec

Title: US-09-970-966-214

Perfect score: 1897
Sequence: 1 gccaaactccggaggtctg.....aaaaaaaaaaaaaaaaaaaaa 1897

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 441362 seqs, 15338381 residues

Total number of hits satisfying chosen parameters: 882724

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 08
Maximum Match 100%

Listing first 45 summaries

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2: /cgn2_6/ptodata/1/lna/5B_COMB.seq.*
3: /cgn2_6/ptodata/1/lna/6A_COMB.seq.*
4: /cgn2_6/ptodata/1/lna/6B_COMB.seq.*
5: /cgn2_6/ptodata/1/lna/ptotus_COMB.seq.*
6: /cgn2_6/ptodata/1/lna/backfiles1.seq.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
C 1	56.4	3.0	1872	1 US-08-153-848-39	Sequence 39, Appl
C 2	56.4	3.0	1872	3 US-09-299-843A-39	Sequence 39, Appl
C 3	56.4	3.0	1872	4 US-09-088-337B-39	Sequence 39, Appl
C 4	56.4	3.0	1872	5 PCT-US93-11153-39	Sequence 39, Appl
C 5	55.6	2.9	477	4 US-09-135-994-1	Sequence 1, Appl
C 6	55.4	2.9	1028	4 US-08-118-200-1	Sequence 1, Appl
C 7	55.4	2.9	1028	4 US-08-458-745-1	Sequence 1, Appl
C 8	50.8	2.7	10348	2 US-08-457-273B-41	Sequence 41, Appl
C 9	50.8	2.7	10348	3 US-08-556-419-13	Sequence 13, Appl
C 10	50.8	2.7	10348	4 US-09-041-886-14	Sequence 14, Appl
C 11	50.8	2.7	10366	1 US-08-246-982A-5	Sequence 5, Appl
C 12	50.8	2.7	10366	1 US-08-453-265-5	Sequence 5, Appl
C 13	50.4	2.7	7218	1 US-08-232-463-14	Sequence 14, Appl
C 14	50.2	2.6	4403765	4 US-09-103-840A-2	Sequence 2, Appl
C 15	50.2	2.6	4411529	4 US-09-103-840A-1	Sequence 1, Appl
C 16	50.2	2.6	63729	1 US-08-499-215-1	Sequence 1, Appl
C 17	49.4	2.6	7218	1 US-08-232-463-14	Sequence 14, Appl
C 18	49.2	2.6	4362	2 US-08-455-073A-1	Sequence 1, Appl
C 19	47.2	2.5	2625	4 US-09-245-041-18	Sequence 18, Appl
C 20	47.2	2.5	3765	3 US-07-705-490-1	Sequence 1, Appl
C 21	47.2	2.5	3765	4 US-07-751-891B-1	Sequence 1, Appl
C 22	47.2	2.5	4072	4 US-09-245-041-16	Sequence 16, Appl
C 23	47.2	2.5	8589	4 US-09-245-041-14	Sequence 14, Appl
C 24	47.2	2.5	4403765	4 US-09-103-840A-2	Sequence 2, Appl
C 25	46.8	2.5	2846	4 US-09-613-182-5	Sequence 5, Appl
C 26	46.6	2.5	1176	4 US-09-200-090-3	Sequence 3, Appl
C 27	46	2.4	289	4 US-09-007-005-17	Sequence 17, Appl

28	46	2.4	289	4 US-09-244-796-17	Sequence 17, Appl
29	45.8	2.4	4362	2 US-08-455-073A-1	Sequence 1, Appl
30	45.6	2.4	1051	4 US-09-245-041-10	Sequence 10, Appl
C 31	45.6	2.4	1342	3 US-08-832-399-1	Sequence 1, Appl
C 32	45.6	2.4	1342	4 US-09-372-498-1	Sequence 1, Appl
C 33	45.6	2.4	1575	3 US-08-858-876A-1	Sequence 1, Appl
C 34	45.6	2.4	1575	4 US-09-472-880-1	Sequence 1, Appl
C 35	45.6	2.4	2419	4 US-09-245-041-8	Sequence 8, Appl
36	45.6	2.4	3000	4 US-08-460-269C-5	Sequence 5, Appl
37	45.6	2.4	8827	4 US-09-245-041-1	Sequence 1, Appl
38	45.4	2.4	4257	2 US-08-690-473-1	Sequence 1, Appl
39	45.4	2.4	4257	4 US-09-259-821A-1	Sequence 1, Appl
40	45.4	2.4	4257	4 US-08-843-659-1	Sequence 1, Appl
C 41	45.4	2.4	12001	1 US-08-458-568A-11	Sequence 11, Appl
C 42	44.8	2.4	700	4 US-09-236-097-7	Sequence 7, Appl
C 43	44.8	2.4	1071	2 US-08-997-080-180	Sequence 180, App
C 44	44.8	2.4	1071	2 US-08-997-362-180	Sequence 180, App
C 45	44.8	2.4	1071	4 US-09-095-855-180	Sequence 180, App

ALIGNMENTS

RESULT 1
US-08-153-848-39/c
Sequence 39, Application US/08153848
Patent No. 5759804
GENERAL INFORMATION:
APPLICANT: Godiska, Ronald
APPLICANT: Gray, Patrick W.
APPLICANT: Schwellkart, Vicki L.
TITLE OF INVENTION: No. 5759804el Seven Transmembrane Receptors
NUMBER OF SEQUENCES: 64
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
ADDRESSEE: Bicknell
STREET: 6300 Sears Tower, 233 South Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/153,848
FILING DATE:
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/977,452
FILING DATE: 17-NOV-1992
ATTORNEY/AGENT INFORMATION:
NAME: No. 5759804and, Greta E.
REGISTRATION NUMBER: 35,302
REFERENCE/DOCKET NUMBER: 31794
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 474-6300
TELEFAX: (312) 474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 39:
SEQUENCE CHARACTERISTICS:
LENGTH: 1872 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
FEATURE:
NAME/KEY: CDS
LOCATION: 202..1341
US-08-153-848-39

CLASSIFICATION:
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 07/977,452
FILING DATE: 17-NOV-1992
ATTORNEY/AGENT INFORMATION:
NAME: Noland, Greta E.
REGISTRATION NUMBER: 35,302
REFERENCE/DOCKET NUMBER: 31794
TELECOMMUNICATIONS INFORMATION:
TELEPHONE: (312) 474-6300
TELEFAX: (312) 474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 39:
SEQUENCE CHARACTERISTICS:
LENGTH: 1872 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
FEATURE:
NAME/KEY: CDS
LOCATION: 202..1341

[illegible]

GENERAL INFORMATION:

APPLICANT: SUTHERLAND, Grant R

APPLICANT: RICHARDS, Robert I

APPLICANT: SCHLESSINGER, David

APPLICANT: NAGARAJA, Ramalah


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? MEDIUM TYPE: Floppy disk
? COMPUTER: IBM PC compatible
? OPERATING SYSTEM: PC-DOS/MS-DOS
? SOFTWARE: Patentin Release #1.0, Version #1.25
? CURRENT APPLICATION DATA:
? APPLICATION NUMBER: US/08/232,463
? FILING DATE:
? CLASSIFICATION: 435
? PRIOR APPLICATION DATA:
? APPLICATION NUMBER: US/07/935,313
? FILING DATE:
? APPLICATION NUMBER: EP 91 114 300.6
? FILING DATE: 26-AUG-1991
? ATTORNEY/AGENT INFORMATION:
? NAME: BENT, Stephen A.
? REGISTRATION NUMBER: 29,768
? REFERENCE/DOCKET NUMBER: 30472/114 IMMU
? TELECOMMUNICATION INFORMATION:
? TELEPHONE: (703)836-9300
? TELEFAX: (703)683-4109
? TELEX: 899149
? INFORMATION FOR SEQ ID NO: 14:
? SEQUENCE CHARACTERISTICS:
? LENGTH: 7218 base pairs
? TYPE: nucleic acid
? STRANDEDNESS: single
? TOPOLOGY: linear
? IMMEDIATE SOURCE:
? CLONE: pTZgpt-Fls
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US-08-232-463-14

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Matches 9; Conservative 221; Mismatches 152; Indels 0; Gaps 0;

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OY 509 TACCACTCCTTCTGCTGCCAGGAACTGAACTCAGTTGGCATCAGCTGCACAC 568
    : : : : : : : : : : : : : : : : : : : : : : : : : :
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OY 569 CCTCTTGAACGGGCCCAAGGCCCAAGAAAGGAGAGTTCTGCGCCCTCAGGCCA 628
    1182 YYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYY 1241
OY 629 GGGCTCCGACACCATCCTGTTCTCTCAAAATAGCCCTCTCTCGGCACACGCGGAAGC 688
    : : : : : : : : : : : : : : : : : : : : : : : : : :
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RESULT 14
US-09-103-840A-2
? Sequence 2, Application US/09103840A
? Patent No. 6294328
? GENERAL INFORMATION:
? APPLICANT: FLEISCHMAN, Robert D.
? APPLICANT: WHITE, Owen R.
? APPLICANT: FRASER, Claitre M.
? APPLICANT: VENTER, John C.

```

```

/ TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM
/ FILE REFERENCE: 24366-20007.00
/ CURRENT APPLICATION NUMBER: US/09/103,840A
/ NUMBER OF SEQ ID NOS: 2
/ SOFTWARE: PatentIn Ver. 2.1
/ SEQ ID NO 2
/ LENGTH: 4403765
/ TYPE: DNA
/ ORGANISM: Mycobacterium tuberculosis
/ FEATURE:
/ OTHER INFORMATION: CDC 1551
/ OTHER INFORMATION: "n" bases at various positions throughout the sequence
US-09-103-840A-2

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Best Local Similarity 51.1%; Score 50.2; DB 4; Length 4403765;
Matches 118; Conservative 0; Mismatches 113; Indels 0; Gaps 0

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QY 85 ATGCAAGCTTCCGCGAGCGCACCTCGTGCGCTCTGATTAGCATCCGCTCTCCGCGGC 144
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Db 338536 CCCCAGCGGCGCCCGAACACACTGCGGCGGCGCCCGCGCGCGCGCGCGCGCGCGC 338595
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QY 145 AGCAAGCGCGGCGCCCAAGACAGCTTGGCAGACACAGCCGCTGCAGCGCGGAGACCTTCGC 204
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Db 338596 CCGGTGTGCGCTCTGATGATCGCTTGCCTTCGCCGCGCGCGCGCGCGCGCGCGCGCGC 338655
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QY 205 TCGTGTGCGCTCTCTGATGATCGCTTGCCTTCGCCGCGCGCGCGCGCGCGCGCGCGCG 255
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RESULT 15
US-09-103-840A-1
/ Sequence 1, Application US/09103840A
/ Patent No. 6294328
/ GENERAL INFORMATION:
/ APPLICANT: FLEISCHMAN, Robert D.
/ APPLICANT: WHITE, Owen R.
/ APPLICANT: FRASER, Claire M.
/ APPLICANT: VENTER, John C.
/ TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM
/ FILE REFERENCE: 24366-20007.00
/ CURRENT APPLICATION NUMBER: US/09/103,840A
/ CURRENT FILING DATE: 1998-06-24
/ NUMBER OF SEQ ID NOS: 2
/ SOFTWARE: PatentIn Ver. 2.1
/ SEQ ID NO 1
/ LENGTH: 4411529
/ TYPE: DNA
/ ORGANISM: Mycobacterium tuberculosis
/ OTHER INFORMATION: H37Rv
US-09-103-840A-1

Query Match
Best Local Similarity 51.1%; Score 50.2; DB 4; Length 4411529;
Matches 118; Conservative 0; Mismatches 113; Indels 0; Gaps 0;

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QY 85 ATGCAAGCTTCCGCGAGCGCACCTGCGGCTCTCTTAAGCTACGACGCGTGCATTCGCGGCGC 144
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Oy	241	GCCCGGGAGCTCCGGAGAAATGTGGTCTCAGGACATCGGGCAACTTTTGGGATGTT	300
Db	241	GCCCGGGAGCTCCGGAGAAATGTGGTCTCAGGACATCGGGCAACTTTTGGGATGTT	300
Oy	301	CTTGCTTCCAGGCTTTGGCGCTGCAGAAATCCAGTGTACAGTGTGAAGAAATTCAGCTGAA	360
Db	301	CTTGCTTCCAGGCTTTGGCGCTGCAGAAATCCAGTGTACAGTGTGAAGAAATTCAGCTGAA	360
Oy	361	CAAGACATGCTCTCCGCCGAGTTCATTTGAATTTGACAGGTGAACGTTCAGAGACATG	420
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Db	601	GGGAAATTCTACCTCTCGGCGCTCAGGGCCAGGGCTCCGACACCAATCTTTCTCTCAAAAT	660
Oy	661	AGCCTCTTCTCGGCACATGCTGTAAGCTGAAGAAATGCAACCCCTCTCTCATTTGTC	720
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Oy	781	ATTCTGGGTAGGAGACGGAGATCCGTTCTCTTTGTCTCTGTGCAAAATTAAGAAG	840
Db	781	ATTCTGGGTAGGAGACGGAGATCCGTTCTCTTTGTCTCTGTGCAAAATTAAGAAG	840
Oy	841	CTCGGTAAAGCATTTCTGAATTAATTCAAGTGAATTTTCAATTAATTAAGAAGA	900
Db	841	CTCGGTAAAGCATTTCTGAATTAATTCAAGTGAATTTTCAATTAATTAAGAAGA	900
Oy	901	AGGAGGTGAGTGAAGATCAACCCCACTGCTGTGAACCGGAGTCAAGGCCAGGCTGGC	960
Db	901	AGGAGGTGAGTGAAGATCAACCCCACTGCTGTGAACCGGAGTCAAGGCCAGGCTGGC	960
Oy	961	AGAGTCMTCTCTTGAAGTCACTGAGTGGGCACTGCTTTTGTAAACCTCCAGTGTG	1020
Db	961	AGAGTCMTCTCTTGAAGTCACTGAGTGGGCACTGCTTTTGTAAACCTCCAGTGTG	1020
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Db	1081	GGCTGGAGGGCAATTTCCCACTCAAGGCTCCCTGCTGTACATTCAAATTTATGCTCT	1140
Oy	1141	GAAGAACCTTCTGACAGCAAAATTTGGCTGTTTCCGCTGAGTTGGGCTCTAGTACT	1200
Db	1141	GAAGAACCTTCTGACAGCAAAATTTGGCTGTTTCCGCTGAGTTGGGCTCTAGTACT	1200
Oy	1201	CGAGACTCAATGACTGGGACTTAGACTGGGGCTCGGCTCTGTAAGAGTCTTAAGA	1260
Db	1201	CGAGACTCAATGACTGGGACTTAGACTGGGGCTCGGCTCTGTAAGAGTCTTAAGA	1260
Oy	1261	AAATCTTCTCAGTTCTCTCTTGACAGAGACTGCGCCGGGACGGAAAGCAACGCGGCT	1320

Db	1261	AAATCTTCTCAGTTCCTCTCTTGACAGSAGACTGCGCGGGACCGGAAGACAAACGGCGCT	1320
OY	1321	GCACAAACCGGGCGCTGTCGCTGGAGTGGCCATGTACGCCGACAGCGCTTCTGTGTG	1380
Db	1321	GCACAAACCGGGCGCTCTCGCTGGAGTGGCCATGTACGCCGACAGCGCTTCTGTGTG	1380
OY	1381	TGGCGTGTGACGAGACAGCGCGGACACAGCACTGCACAAACCCGCGAAATCTCT	1440
Db	1381	TGGCGTGTGACGAGACAGCGCGGACACAGCACTGCACAAACCCGCGAAATCTCT	1440
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OY	1501	AGAAAGGAGAGAGATATATGTACGCCCGGAAGTAGAAGCTGTCCAGTCTGCTGGGTT	1560
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OY	1561	TGGCGCGAGCCATGATCCTCCGAATCTGTGTGGGCATCCAGATACGGCCATGTACAA	1620
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OY	1621	CAATCAGCCCTGGGCAACACACGACGAGGAGGAGACAGACAGAAAAAAGAAAAACACAGAT	1680
Db	1621	CAATCAGCCCTGGGCAACACACGACGAGGAGGAGAGACAGAAAAAAGAAAAACACAGAT	1680
OY	1681	GAGAAACACAGTAATGATATAAACCATTAATATTATGACCCCTCTGTCTGTCTTACTG	1740
Db	1681	GAGAAACACAGTAATGATATAAACCATTAATATTATGACCCCTCTGTCTGTCTTACTG	1740
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Db	1741	GCCAGGAAATGATCCCAATTTTTCAGTGTGACCTGACAGCTTCTTTTGCACAAAGAA	1800
OY	1801	GAGAGAAATTTAAACACTCTTTCAAAACCCGGGGAGTGGCTGTGTAAAGAAAGACATTA	1860
Db	1801	GAGAGAAATTTAAACACTCTTTCAAAACCCGGGGAGTGGCTGTGTAAAGAAAGACATTA	1860
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RESULT 2
; US-09-825-294-205
; Sequence 205, Application US/09825294
; Patent No. US20020004491A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Stolk, John A.
; APPLICANT: Algate, Paul A.
; APPLICANT: Fling, Steven P.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
; TITLE OF INVENTION: THERAPY AND DIAGNOSIS OF OVARIAN CANCER
; FILE REFERENCE: 210121.484C5
; CURRENT APPLICATION NUMBER: US/09/825,294
; CURRENT FILING DATE: 2001-04-03
; NUMBER OF SEQ ID NOS: 215
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 205
; LENGTH: 1619
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-825-294-205

Query Match      84.7%  Score 1606, 2;  DB 10;  Length 1619;
Best Local Similarity 99.8%  Pred. No. 0;
Matches 1616;  Conservative 2;  Mismatches 0;  Indels 1;  Gaps 1;

Oy      280  GGCACCTTTTGGGATGTGTTCTCTCCACAGCCTTTGGGCGCAAAATCCAGTGTACCA 339
Db      1    GGCACCTTTTGGGATGTGTTCTCTCCACAGCCTTTGGGCGCAAAATCCAGTGTACCA 60

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OY 340 GTGTGAAGAAATCCAGCTGAACAAGACTGCMCTCCCCGAGTTCAATTGTGAATTCAC 399
    |||||||
DB 61 GTGTGAAGAAATCCAGCTGAACAAGACTGCTCTCTCCCCGAGTTCAATTGTGAATTCAC 120
OY 400 GTGTGAAGAAATCCAGCTGAACAAGACTGCMCTCCCCGAGTTCAATTGTGAATTCAC 459
    |||||||
DB 121 GTGTGAAGAAATCCAGCTGAACAAGACTGCMCTCCCCGAGTTCAATTGTGAATTCAC 180
OY 460 CCGCAATCTCTGTGATCATATGAGGGGCTGTCTCATCCCTCTCTGCGGGTACAGTCTT 519
    |||||||
DB 181 CCGCAATCTCTGTGATCATATGAGGGGCTGTCTCATCCCTCTCTGCGGGTACAGTCTT 240
OY 520 CTCTCCCAAGGAAATGAACTGATGATGATGATGATGATGATGATGATGATGATGAT 579
    |||||||
DB 241 CTCTCCCAAGGAAATGAACTGATGATGATGATGATGATGATGATGATGATGATGAT 300
OY 580 CCGGCAAGGAAATGAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 639
    |||||||
DB 301 CCGGCAAGGAAATGAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 360
OY 640 CACCATCTGTCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 699
    |||||||
DB 361 CACCATCTGTCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 420
OY 700 CCAACCCCTCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 759
    |||||||
DB 421 CCAACCCCTCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 480
OY 760 GTTCTCTCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 819
    |||||||
DB 481 GTTCTCTCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 540
OY 820 CCGTGAAGAAATGAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 879
    |||||||
DB 541 CCGTGAAGAAATGAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 600
OY 880 TTTTCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 939
    |||||||
DB 601 TTTTCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 660
OY 940 CCGAGTCAAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 999
    |||||||
DB 661 CCGAGTCAAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 720
OY 1000 TTTTGAAGAAATGAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1059
    |||||||
DB 721 TTTTGAAGAAATGAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 780
OY 1060 GTGAGAGTACGTTTCTTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1119
    |||||||
DB 781 GTGAGAGTACGTTTCTTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 840
OY 1120 ACATTTCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1179
    |||||||
DB 841 ACATTTCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 900
OY 1180 CTGAGTGTGAGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1239
    |||||||
DB 901 CTGAGTGTGAGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 960
OY 1240 CCGCTCTGAAGAAATGAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1299
    |||||||
DB 961 CCGCTCTGAAGAAATGAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1020
OY 1300 AGCGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1359
    |||||||
DB 1021 AGCGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1080
OY 1360 CCGGCAAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1418
    |||||||
DB 1081 CCGGCAAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1140

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OY 1419 ACGAACCACCCGGAACCTGTGAGAGACACCGTGTACAGAGAGAGAGAGAGAGAG 1478
    |||||||
DB 1141 ACGAACCACCCGGAACCTGTGAGAGACACCGTGTACAGAGAGAGAGAGAGAGAG 1200
OY 1479 CTGAGTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1538
    |||||||
DB 1201 CTGAGTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1260
OY 1539 CTGCTCCAGTGTGCTTGGGTTTGGCCGACAGCCATGATCCCTCCGATCTGTGGGATC 1598
    |||||||
DB 1261 CTGCTCCAGTGTGCTTGGGTTTGGCCGACAGCCATGATCCCTCCGATCTGTGGGATC 1320
OY 1599 CACCATACGGCCATATGTCACACATATACCCCTGTGGGAGACAGACAGAGAGAGAG 1658
    |||||||
DB 1321 CACCATACGGCCATATGTCACACATATACCCCTGTGGGAGACAGACAGAGAGAGAG 1380
OY 1659 AGAGAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1718
    |||||||
DB 1381 AGAGAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1440
OY 1719 CCCCTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCT 1778
    |||||||
DB 1441 CCCCTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCT 1500
OY 1779 CAGCTCTTTGGCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1838
    |||||||
DB 1501 CAGCTCTTTGGCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1560
OY 1839 CTGTGTAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1897
    |||||||
DB 1561 CTGTGTAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1619

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RESULT 3
US-09-825-294-211
; Sequence 211, Application US/09825294
; Patent No. US20020004491A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Stolk, John A.
; APPLICANT: Algate, Paul A.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
; FILE OF INVENTION: THERAPY AND DIAGNOSIS OF OVARIAN CANCER
; FILE REFERENCE: 210121.484C5
; CURRENT APPLICATION NUMBER: US/09/825, 294
; CURRENT FILING DATE: 2001-04-03
; NUMBER OF SEQ ID NOS: 215
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 211
; LENGTH: 1619
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-825-294-211

```

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Query Match      84.7%: Score 1606.2: DB 10: Length 1619:
Best Local Similarity 99.8%: Pred. No. 0:
Matches 1616: Conservative 2: Mismatches 0: Indels 1: Gaps 1:

OY 280 GCGCACTTTTGGAGATGTTCTGTCTCCAGGCTTTGGCTCCAAATCCAGTGTACCA 339
    |||||||
DB 1 GCGCACTTTTGGAGATGTTCTGTCTCCAGGCTTTGGCTCCAAATCCAGTGTACCA 60
OY 340 GTGTGAAGAAATCCAGCTGAACAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 399
    |||||||
DB 61 GTGTGAAGAAATCCAGCTGAACAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 120
OY 400 GTGTGAAGAAATCCAGCTGAACAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 459
    |||||||
DB 121 GTGTGAAGAAATCCAGCTGAACAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 180
OY 460 CCGCAAGTCTGTGATCATACAGGCGCTGTCTCATCGGCTGTGCGGGTACCAAGTCTT 519
    |||||||

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Db 181 CCGAAGTCCTGTGATGATCAGGGGCTGTCTATGCTCTGTGCGGGGTACAGATCTT 240
OY 520 CTGCTCCCGAGGAACTGAACCTGATTGATCAGCTGCTGCAACACCCCTCTTTGTA 579
Db 241 CTGCTCCCGAGGAACTGAACCTGATTGATCAGCTGCTGCAACACCCCTCTTTGTA 300
OY 580 CGGGCCAAAGGCCCCAAGAAAGGGAAGTTGCGCTCGGCGCTCAGAGGCGCTCGGAC 639
Db 301 CGGGCCAAAGGCCCCAAGAAAGGGAAGTTGCGCTCGGCGCTCAGAGGCGCTCGGAC 360
OY 640 CACCATCTGTTCTCTCAAAATTAAGCCCTCTTCTCGGACACCTGCTGAAGCTGAAGAGATG 699
Db 361 CACCATCTGTTCTCTCAAAATTAAGCCCTCTTCTCGGACACCTGCTGAAGAGATG 420
OY 700 CCACCCCTCTGCTGATTTCTCTCCAGCCCTCGCCCAACCCCGCCACTCCCTGAGTA 759
Db 421 CCACCCCTCTGCTGATTTCTCTCCAGCCCTCGCCCAACCCCGCCACTCCCTGAGTA 480
OY 760 GTTCTCTGCTGCTGCTCTTTATTTCTGAGGAGGAGGAGTCCGCTCTTTGTT 819
Db 481 GTTCTCTGCTGCTGCTCTTTATTTCTGAGGAGGAGGAGTCCGCTCTTTGTT 540
OY 820 CCTGTCAAAATTAAGAAAGCTGCTGAAGCATTTCTGAATTAATTCAGCTGACTGAAT 879
Db 541 CCTGTCAAAATTAAGAAAGCTGCTGAAGCATTTCTGAATTAATTCAGCTGACTGAAT 600
OY 880 TTTCACTGATGATGATGAAGAAAGGAGGAGTGAAGTTCACCCCAATGCTGTGTATAC 939
Db 601 TTTCACTGATGATGATGAAGAAAGGAGGAGTGAAGTTCACCCCAATGCTGTGTATAC 660
OY 940 CGGAGTCAAGGCGCAGAGCTGCGAGAGTCTGCTTGAAGTCACTAGAGTGGGATCTGCC 999
Db 661 CGGAGTCAAGGCGCAGAGCTGCGAGAGTCTGCTTGAAGTCACTAGAGTGGGATCTGCC 720
OY 1000 TTTTAAAGCTCCAGTGTCTCATTCCTGATGGGGGATGTTTGAAGTGCAGA 1059
Db 721 TTTTAAAGCTCCAGTGTCTCATTCCTGATGGGGGATGTTTGAAGTGCAGA 780
OY 1060 GTGAGAGTACGCTTTCTAGAGGCTGGAAGGCGAGTCCCACTCAAGGCTCCCTGCTTG 1119
Db 781 GTGAGAGTACGCTTTCTTAGAGGCTGGAAGGCGAGTCCCACTCAAGGCTCCCTGCTTG 840
OY 1120 ACATTCAAACTTCATGCTCTGAAAAACCAATTCCTGACAGCAGAAATTTGGCTTTCGCGC 1179
Db 841 ACATTCAAACTTCATGCTCTGAAAAACCAATTCCTGACAGCAGAAATTTGGCTTTCGCGC 900
OY 1180 CTGAGTTGGGCTCTAGTACTGAGACTCAATGACTGGGACTTAAGCTGGGCTCGGCT 1239
Db 901 CTGAGTTGGGCTCTAGTACTGAGACTCAATGACTGGGACTTAAGCTGGGCTCGGCT 960
OY 1240 CGCTGTGAAGAGTGTGAAGAAATCTCTCAGTTCTCTTGCAGAGGAGCTGGCGCGG 1299
Db 961 CGCTGTGAAGAGTGTGAAGAAATCTCTCAGTTCTCTTGCAGAGGAGCTGGCGCGG 1020
OY 1300 ACGCAGAGCAAGCGGGGCTGACAAAACCGGGGCTGTGCGGTGTGAAGTGCAGATGA 1359
Db 1021 ACGCAGAGCAAGCGGGGCTGACAAAACCGGGGCTGTGCGGTGTGAAGTGCAGATGA 1080
OY 1360 CGCGCAGGCGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1418
Db 1081 CGCGCAGGCGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1140
OY 1419 ACGAAGACCGCGGAGAACTGCTGAGAGCAACCTGTATACAGAGCGGGTGTGAAGCAG 1478
Db 1141 ACGAAGACCGCGGAGAACTGCTGAGAGCAACCTGTATACAGAGCGGGTGTGAAGCAG 1200
OY 1479 CTGAGGTAGAAAAGCTCTCCGAGAGAGGAGAGATCATGTACGCCCGGAGTAGAGAC 1538
Db 1201 CTGAGGTAGAAAAGCTCTCCGAGAGAGGAGAGATCATGTACGCCCGGAGTAGAGAC 1260
OY 1539 CTGCTGCAAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1598
Db 1261 CTGCTGCAAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1320

OY 1599 CAGCATACGGCCAAATGTACAAACATTCAGCCCTGGGACAGACAGAGAGAGAGAC 1658
Db 1321 CAGCATACGGCCAAATGTACAAACATTCAGCCCTGGGACAGACAGAGAGAGAGAC 1380
OY 1659 AGAGAAAAGAAAACACAGCATGAGACAGTAAATGAATTAATTAATTTAG 1718
Db 1381 AGAGAAAAGAAAACACAGCATGAGACAGTAAATGAATTAATTAATTTAG 1440
OY 1719 CCCCTGTGTCTGTCTTACTGCGCAGAAATGTACAAATTTTACGTGTGACTGA 1778
Db 1441 CCCCTGTGTGTGTCTTACTGCGCAGAAATGTACAAATTTTACGTGTGACTGA 1500
OY 1779 CAGCTTCTTTTCCCAAGCAAGAGAGAAATTTAACAATGTTTCAAAACCCGGGAGTTGG 1838
Db 1501 CAGCTTCTTTTCCCAAGCAAGAGAGAAATTTAACAATGTTTCAAAACCCGGGAGTTGG 1560
OY 1839 CTGTGTTAAGAAAGACATTAATGCTTTTACAGCTGTATATATATATATATATAT 1897
Db 1561 CTGTGTTAAGAAAGACATTAATGCTTTTACAGCTGTATATATATATATATATAT 1619

RESULT 4

US-09-825-294-210
; Sequence 210, Application US/09825294
; Patent No. US2002000491A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Stolk, John A.
; APPLICANT: Algate, Paul A.
; APPLICANT: Filing, Steven P.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
; FILE REFERENCE: 210121.484C5
; CURRENT APPLICATION NUMBER: US/09/825,294
; NUMBER OF SEQ ID NOS: 215
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 210
; LENGTH: 625
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(625)
; OTHER INFORMATION: n = A,T,C or G
US-09-825-294-210

Query Match 32.9%; Score 624; DB 10; Length 625;
Best Local Similarity 99.8%; Pred. No. 7.2e-154;
Matches 624; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1271 AGTTCTCTCTTGTGAGAGTGTGCGCGCGGAGCGGAGAGCAAGAGCGGCTGCAAAAGCG 1330
Db 1 AGTTCTCTCTTGTGAGAGTGTGCGCGCGGAGCGGAGAGCAAGAGCGGCTGCAAAAGCG 60
OY 1331 GCGCGCTGT 1390
Db 61 GCGCGCTGT 120
OY 1391 CAGCGACAGGCGGACAGACAGTGTGACAGCAACACCCCGGAACTGCTGAGAGACAC 1450
Db 121 CAGCGACAGGCGGACAGACAGTGTGACAGCAACACCCCGGAACTGCTGAGAGACAC 180
OY 1451 CGTGTACAGAGCGGGTGTATGACGAGCTGAGGTGAAGAAAGCTTCGAGAGAGGAG 1510
Db 181 CGTGTACAGAGCGGGTGTATGACGAGCTGAGGTGAAGAAAGCTTCGAGAGAGGAG 240
OY 1511 GAGGATCATGTACGCCCGGAGTAGAGCTGTCTGCTGCTGCTGCTGCTGCTGCTGCTG 1570
Db 241 GAGGATCATGTACGCCCGGAGTAGAGCTGTCTGCTGCTGCTGCTGCTGCTGCTGCTG 300
OY 1571 CATGATCTCCGAATCTGTTGGGATTCAGACATACGCCCAATGTTCACAAATCAAGCC 1630

QY	1571	CAGATCTCTCGGAAATCTGTGTTGGGCATCCAGCATACGCCCAATGTCACCAATCAGCC	16330
Db	301	CATGATCTCTCGGAATCTGTGTTGGGCATCCAGCATACGCCCAATGTCACCAATCAGCC	360
QY	1631	TGGGCAGACAGCAGCAGAGGAGGAGACAGACAGAAAAAGAAAAACACAGCATGAGAACACAG	16990
Db	361	TGGGCAGACAGCAGCAGAGGAGGAGAGACAGAGAAAAAGAAAAACACAGCATGAGAACACAG	420
QY	1691	TAAATGATTAATAAACATTAATAATTAATTAAGCCCTCTGTGTGCTTACTGCGCCAGAAAT	1750
Db	421	TAAATGATTAATAAACATTAATAATTAATTAAGCCCTCTGTGTGCTTACTGCGCCAGAAAT	480
QY	1751	GGTACCAATTTTTCACTGTGTGACCTTGACAGCTCTTTTGGCACAAGCAGAGAGAAATTT	1810
Db	481	GGTACCAATTTTTCACTGTGTGACCTTGACAGCTCTTTTGGCACAAGCAGAGAGAAATTT	540
QY	1811	AACACTTTTCAAAACCGGGGAGTTGGCGTGTTAAGAGAAAGACCATTAATAGCTTAAAG	1870
Db	541	AACACTTTTCAAAACCGGGGAGTTGGCGTGTGTTAAGAGAAAGACCATTAATAGCTTAAAG	600
QY	1871	ACAGGTAAATAAAAAAAAAAAAAA 1895	
Db	601	ACAGGTAAATAAAAAAAAAAAAAA 625	

```

RESULT 6
US-09-825-294-212
; Sequence 212: Application US/09825294
; Patent No. US20020004491A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Stolk, John A.
; APPLICANT: Algate, Paul A.
; APPLICANT: Flind, Steven P.
; TITLE OF INVENTION: THERAPY AND METHODS FOR THE
; TREATMENT OF OVARIAN CANCER
; FILE REFERENCE: 210121.484C5
; CURRENT APPLICATION NUMBER: US/09/825, 294
; CURRENT FILING DATE: 2001-04-03
; NUMBER OF SEQ ID NOS: 215
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 212
; LENGTH: 1010
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-09-825-294-212

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Query Match	Best Local Similarity	29.9%;	Score 566.4;	DB 10;	Length 1010;
Matches	687;	Conservative	0;	Mismatches 31;	Indels 12;
					Gaps 9;
QY	58	CCGCAGCCGGAGACCCGACAGCCGGGGCCATGCAAGGCTCCGCGAGAGGGACACTGCGGCTCCT	117		
Db	1	CCGCAGCCGGAGAGCCGACAGCGGGGGCCATGCAAGGCTCCGCGAGAGGGACACTGCGGCTCCT	117		
QY	118	CTAAGCTACACACCGTGTCTCTCCGC -GGCAGCAGC -GGCGGGGCCACAGCAGCTCGCAGCC	175		
Db	61	CTAAGCTACACACCGTGTCTCTCCGCAGCAGCAGCTCGCGGGGCCACAGCCTCGGCAACC	120		
QY	176	ACAGCGGCTGCAGCC -GGGCGAGCCTCGGTGCTGTGCGCTCTCTGTATGGCTTGGCCT	234		
Db	121	ACAGCGGCTGCAGCCGTGGGGGCGAGCCTCGCGTGTGCGCTCTGTATGGCTTGGCCT	180		
QY	235	CTTCCC -GGCCCCGGGAGCTCGGGGAGATGTGGGCTCTAAGCATGCGGGCAACTTTTTCGG	293		
Db	181	CTTCCCCTGGCCCCGGGAGCTCGGGGAGATGTGGGCTCTAAGCATGCGGGCAACTTTTTCGG	240		
QY	294	GATTGTTCTTGCTTC -AGGCTTTGGGCTTCCAATCCAGTGTACCAAGTGTGAAGAATTC	352		
Db	241	GATTGTTCTTGCTTCCAAGCTTTGGGCTTCCAATCCAGTGTACCAAGTGTGAAGAATTC	300		
QY	353	CAGCTAACACAGACGTCTCTCCCGAGATTATTGTGAATTGCACAGGTGAAGCTTCAA	412		

Db 301 CAGCTGACAAAGACTGCTCCCTCCCGAGTTTCATTGTGAATTGCAAGGTTGAAAGTTTCAA 360
 413 GACATGTGTGCAAGAAAGATGATGAGCAAAAGGCGGATCATGTACCCAGATCCTGT 472
 Db 361 GACATGTGTGCAAGAAAGATGATGAGCAAAAGGCGGATCATGTACCCAGATCCTGT 420
 473 GCATCATCAGAGGCTGTCTCATCGCTTCCGCGGATACAGTCTTCTGTCTCCAGGG 532
 Db 421 GCATCATCAGAGGCTGTCTCATCGCTTCCGCGGATACAGTCTTCTGTCTCCAGGG 480
 533 AAACGTACATCAGTTTTCATCAGTGTGTGCAACACCCCTCTTTTCTAA-CCGGGCAAGGCC 591
 Db 481 AAACGTACATCAGTTTTCATCAGTGTGTGCAACACCCCTCTTTTCTAA-CCGGGCAAGGCC 540
 592 CAGAAAAAGGGAAGTCTGCTGCGGCTCAGGCAAGGCTCCGCAACCATCTCTTT 651
 Db 541 CAGAAAAAGGGAAGTCTGCTGCGGCTCAGGCAAGGCTCCGCAACCATCTCTTT 600
 652 CCTCAAAATTA--GCCCTCTTCTCGGCAACACTGTGAA--GCTGAAGAGATGCCACCCC 706
 Db 601 CCTCAAAATTAAGCCCTACTTCTCGGCAACACTGTGAAAGTGAAGGAGGACACCCA 660
 707 CTCTGCTATGTCTTCTTCAGGCTCCGCGGCTCCCAACCCCTGAGTGAAGTCTTCT 766
 Db 661 CTCTGCTATGTCTTCATCAGGCTCGGCTCCGCAACACCCA-CTCCCTGAGAGAGACGCGC 719
 767 CTGGGTGTC 776
 Db 720 CAGGAGAGCC 729

RESULT 7

US-09-825-294-208/c
 : Sequence 208, Application US/09825294
 : Patent No. US20020004491A1
 : GENERAL INFORMATION:
 : APPLICANT: Xu, Jiangchun
 : APPLICANT: Stolck, John A.
 : APPLICANT: Algate, Steven P.
 : APPLICANT: Filing, Steven P.
 : TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
 : TITL OF INVENTION: THERAPY AND DIAGNOSIS OF OVARIAN CANCER
 : FILE REFERENCE: 210121.484C5
 : CURRENT APPLICATION NUMBER: US/09/825.294
 : CURRENT FILING DATE: 2001-04-03
 : NUMBER OF SEQ ID NOS: 215
 : SOFTWARE: FastSeq for Windows Version 3.0
 : SEQ ID NO 208
 : LENGTH: 1362
 : TYPE: DNA
 : ORGANISM: Homo sapiens
 : US-09-825-294-208

Query Match 26.8%; Score 508.6; DB 10; Length 1362;
 Best Local Similarity 99.2%; Pred. No. 1.9e-123;
 Matches 511; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1124 TCAAACTTCATGCTCTGAAACCAATTCCTGACAGAAATTCGCTGTTGCGGCTGA 1183
 Db 1362 TCAAACTTCATGCTCTGAAACCAATTCCTGACAGAAATTCGCTGTTGCGGCTGA 1303
 1184 GTTGGGCTCTAGACTCAGACTCAATGACTGAGCTTGAAGTGGGCTCGGCTCGCT 1243
 Db 1302 GTTGGGCTCTAGACTCAGACTCAATGACTGAGCTTGAAGTGGGCTCGGCTCGCT 1243
 1244 CTGAAAGTCTTAAAGAAATCTTCTCAGTCTCTTTCGACAGAGCTGGCGCGGAGAGC 1303
 Db 1242 CTGAAAGTCTTAAAGAAATCTTCTCAGTCTCTTTCGACAGAGCTGGCGCGGAGAGC 1183
 1304 GAAGAGCAACGGGCTGCAAAAGGCGGCTGTGGGCTGGGAGGAGGAGGAGGAGGAGG 1363
 Db 1182 GAAGAGCAACGGGCTGCAAAAGGCGGCTGTGGGCTGGGAGGAGGAGGAGGAGGAGG 1123

QY 1364 CAGCGCTTCTCGTGGTGTGGCTGCTGACAGAGGCGGCGAGACAGCACTTCACAGAA 1423
 Db 1122 CAGCGCTTCTCGTGGTGTGGCTGCTGACAGAGGCGGCGAGACAGCACTTCACAGAA 1063
 1424 CACCGCGGAAATCTGTCGAGAGACACCGGTACAGAGCGGGTGTATGACCGAGCTGAG 1483
 Db 1062 CACCGCGGAAATCTGTCGAGAGACACCGGTACAGAGCGGGTGTATGACCGAGCTGAG 1003
 1484 GTAGAAAAAGCTCTCCAGAAAGGAGGAGAGATGATGAGCCCGGAAAGTGAAGTCTGT 1543
 Db 1002 GTAGAAAAAGCTCTCCAGAAAGGAGGAGATGATGAGCCCGGAAAGTGAAGTCTGT 943
 1544 CCACTGCTGCTTGGGCTTGGCGGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1603
 Db 942 CCACTGCTGCTTGGGCTTGGCGGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 883
 1604 TACGGCAATGTCAACAAATCAGCCCTGCGGCA 1638
 Db 882 TACGGCAATGTCAACAAATCAGCCCTCAGGAGA 848

RESULT 8

US-09-825-294-213
 : Sequence 213, Application US/09825294
 : Patent No. US20020004491A1
 : GENERAL INFORMATION:
 : APPLICANT: Xu, Jiangchun
 : APPLICANT: Stolck, John A.
 : APPLICANT: Algate, Steven P.
 : APPLICANT: Filing, Steven P.
 : TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
 : TITL OF INVENTION: THERAPY AND DIAGNOSIS OF OVARIAN CANCER
 : FILE REFERENCE: 210121.484C5
 : CURRENT APPLICATION NUMBER: US/09/825.294
 : CURRENT FILING DATE: 2001-04-03
 : NUMBER OF SEQ ID NOS: 215
 : SOFTWARE: FastSeq for Windows Version 3.0
 : SEQ ID NO 213
 : LENGTH: 480
 : TYPE: DNA
 : ORGANISM: Homo sapiens
 : US-09-825-294-213

Query Match 25.1%; Score 476.8; DB 10; Length 480;
 Best Local Similarity 99.6%; Pred. No. 2.2e-115;
 Matches 478; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GCCAATCTCGGAGGCTCTGCTGCTGCGGCGGAGGCGGAGGCGGAGGAGGAGGAGGAGGAG 60
 Db 1 GCCAATCTCGGAGGCTCTGCTGCTGCGGCGGAGGCGGAGGCGGAGGCGGAGGAGGAGGAG 60
 61 CAGCGGAGAGCCCGAGAGCGGCGGAGATGACAGGCTCCGAGAGCGGACCTGCGGCTCTCTA 120
 Db 61 CAGCGGAGAGCCCGAGAGCGGCGGAGATGACAGGCTCCGAGAGCGGACCTGCGGCTCTCTA 120
 121 AGCTACGACCGCTGCTTCCGCGGAGAGAGAGGCGGCGGCGGAGAGGAGGAGGAGGAGGAG 180
 Db 121 AGCTACGACCGCTGCTTCCGCGGAGAGAGAGGCGGCGGCGGAGAGGAGGAGGAGGAGGAG 180
 181 CGCTGAGAGCGGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 240
 Db 181 CGCTGAGAGCGGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 240
 241 GCCCGGAGCTCCGAGAGATGTGGGTCTAGGCAATGCGGCAACTTTTGGGAGATTGT 300
 Db 241 GCCCGGAGCTCCGAGAGATGTGGGTCTAGGCAATGCGGCAACTTTTGGGAGATTGT 300
 301 CTTCCTTCAGAGCTTTCGCTGCAATTCAGTCTACCAATGAGAAATTCAGCTGAA 360
 Db 301 CTTCCTTCAGAGCTTTCGCTGCAATTCAGTCTACCAATGAGAAATTCAGCTGAA 360
 361 CAGGAGTGTCTCCCGGAGTTCAATTGTGAATTGACAGGAGTGAACGTTCAAGACATGTG 420

Db 361 CAAGACTGCTCTCCCGCCGAGTTCATTTGTAATTCAGACGGTGAACGTTTCAAGACATGTG 420
QY 421 TCAGAAAGAGTGTATGAGCAAAAGTCCGGGATCATGTACCGCAAGTCTGTGCATCATC 480
Db 421 TGAGAAAGAGTGTATGAGCAAAAGTCCGGGATCATGTATCCGCAAGTCTGTGCATCATC 480

RESULT 9

US-09-867-701-2375
; Sequence 2375, Application US/09867701
; Patent No. US20020132237A1
; GENERAL INFORMATION:
; APPLICANT: Agiate, Paul A.
; APPLICANT: Jones, Robert
; APPLICANT: Harlocker, Susan L.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE REFERENCE: 210121.497
; CURRENT APPLICATION NUMBER: US/09/867,701
; CURRENT FILING DATE: 2001-05-29
; NUMBER OF SEQ ID NOS: 10912
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2375
; LENGTH: 558
; TYPE: DNA
; ORGANISM: Homo sapien
; FEATURE:
; NAME/KEY: misc.feature
; LOCATION: (1)...(558)
; OTHER INFORMATION: n = A,T,C or G
US-09-867-701-2375

Query Match 22.8%; Score 433.2; DB 10; Length 558;
Best Local Similarity 95.6%; Pred. No. 6.3e-104;

Matches 539; Conservative 0; Mismatches 14; Indels 11; Gaps 9;

QY 1271 AGTTCCTCTTCAGAGAGTGGCGCGGAGCGGAGAGCAACCGGGCGGTGCACAAACCG 1330
Db 1 AGTTCCTCTTCAGAGAGTGGCGCGGAGCGGAGAGCAACCGGGCGGTGCACAAACCG 60
QY 1331 GGGCGGTGCAGTGTGAGTGGCGCATGTACGCGAGCGGCTTCCTGCTGTGGCTGCTG 1390
Db 61 GGGCGGTGCAGTGTGAGTGGCGCATGTACGCG -AGGCGCTTCCTGCTGTGGCTGCTG 118
QY 1391 CACGAGAGCGGCGGAGCAACGACCTTCACAGAACCCCGCGAACTGTCTGCGAGACAC 1450
Db 119 CACGAGAGCGGCGGAGCA -ACAGCACTGTCACAGAACCCCGCGAACTGTCTGCGAGACAC 176
QY 1451 CCGTGTACAGAGCGGCTGTGATGACCGAGCTGAGGTAGAAAAGCTTCGAGAAAGGGAG 1510
Db 177 CCGTGTACAGAGCGGCTGTGATGACCGAGCTGAGGTAGAAAAGCTTCGAGAAAGGGAG 236
QY 1511 GAGGATCATGTACG -CCCGGAAGTAGACCTGTCAGTGCCTGTTGGGTTGGCCGAG 1569
Db 237 GAGGATCATGTACGCGCCCGGAAGTAGACCTGTCAGTGCCTGTTGGGTTGGCCGAG 296
QY 1570 CCATGA -TCCCTCGAATGTGGTGGGATCCAGCATACGGCCCATGTGCACAAACATAGC 1628
Db 297 CATTTATCTCTCGCAATCTGTGTGGGATCCAGCATACGGCCCATGTGCACAAACATAGC 356
QY 1629 CCTGGGCAAGACAGACAGG -AGGAGAGACAGAGAAAAGAAAACACACATGAGAAC 1687
Db 357 CCTGGGCAAGACAGACAGGAGAGAGACAGAAAAGAAAACACACATGAGAAC 416
QY 1688 CAGTAATTAATTAACATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1747
Db 417 CAGTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 474
QY 1748 AATGTACCAATTTTTCAGTGTGAGTGTGACAGCTTCCTTTTCCCAAGCAGAGAGAA 1807
Db 475 AATGTACCAATTTTTCAGTGTGAGTGTGACAGCTTCCTTTTCCCAAGCAGAGAG -A 532
QY 1808 TTTTACACTGTTTCAAAACCGGGG 1831

Db 533 NTTAACATTGTTTCAAAACCGGGG 556

RESULT 10

US-09-867-701-4240/c
; Sequence 4240, Application US/09867701
; Patent No. US20020132237A1
; GENERAL INFORMATION:
; APPLICANT: Agiate, Paul A.
; APPLICANT: Jones, Robert
; APPLICANT: Harlocker, Susan L.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE REFERENCE: 210121.497
; CURRENT APPLICATION NUMBER: US/09/867,701
; CURRENT FILING DATE: 2001-05-29
; NUMBER OF SEQ ID NOS: 10912
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4240
; LENGTH: 409
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-867-701-4240

Query Match 20.9%; Score 396.4; DB 10; Length 409;
Best Local Similarity 99.5%; Pred. No. 2.3e-94;
Matches 408; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

QY 1468 TGATGACCGAGCTGAGTAGAAAAACGTCTCCGAGAGGAGAGAGATCATGTACGCC 1527
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QY 1528 GGAAGTAGAGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1587
Db 349 GGAAGTAGAGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 291
QY 1588 GGTGGGATCAGACATGAGGCGCAATGTCACACAAATAGCCCTGGGAGACAGACAG 1647
Db 290 GGTGGGATCAGACATGAGGCGCAATGTCACACAAATAGCCCTGGGAGACAGACAG 231
QY 1648 GAGGAGAGACAGAAAAAAGAAAAACACAGCATGAGAACACATTAATTAATTAATTAAT 1707
Db 230 GAGGAGAGACAGAAAAAAGAAAAACACAGCATGAGAACACATTAATTAATTAATTAAT 171
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QY 1768 GTTGAGCTGACAGCTTCTTTGCCACAGACAGAGAAATTAATTAATTAATTAATTAAT 1827
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QY 1828 GGGGAGTGTGCTGTGTTAAAGAAACATTAATCTTTAGACAGT 1877
Db 50 GGGGAGTGTGCTGTGTTAAAGAAACATTAATCTTTAGACAGT 1

RESULT 11

US-09-867-701-4251
; Sequence 4251, Application US/09867701
; Patent No. US20020132237A1
; GENERAL INFORMATION:
; APPLICANT: Agiate, Paul A.
; APPLICANT: Jones, Robert
; APPLICANT: Harlocker, Susan L.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE REFERENCE: 210121.497
; CURRENT APPLICATION NUMBER: US/09/867,701
; CURRENT FILING DATE: 2001-05-29
; NUMBER OF SEQ ID NOS: 10912
; SOFTWARE: FastSeq for Windows Version 4.0

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Db	241	CTGCTCCCCAGGGAAGTGAAGTTCAGTTTGATCATCGCTGCACACCCCTCTTTGTAA	300
QY	580	CGGGCCAAAGGCCCAAGAAAGGGAATTTCTGCTCGGCGCTCAGGCGCAGGCTCCGCAC	639
Db	301	CGGGCCAAAGGCCCAAGAAAGGGAAGTTCGCTCCGCGCTCAGGCGCAGGCTCCGCAC	360
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Db	361	CACCATCTT	369

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RESULT 14
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: Sequence 1516, Application US/09867701
: Patent No. US20020132237A1
: GENERAL INFORMATION:
: APPLICANT: Agilate, Paul A.
: APPLICANT: Jones, Robert
: APPLICANT: Harlocker, Susan L.
: TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
: OF OVARIAN CANCER
: FILE REFERENCE: 210121.497
: CURRENT APPLICATION NUMBER: US/09/867,701
: CURRENT FILING DATE: 2001-05-29
: NUMBER OF SEQ. ID NOS.: 10912
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ. ID NO. 1516
: LENGTH: 373
: TYPE: DNA
: ORGANISM: Homo sapien
: US-09-867-701-1516

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Query Match	19.1%	Score 363;	DB 10;	Length 373;
Best Local Similarity	99.7%	Pred. No. 2.2e-85;		
Matches 373;	Conservative 0;	Mismatches 0;	Indels 1;	Gaps 1.

QY	1504	AGGGGAGGAGATCATCTACGCCCGGGAAGTAGACCTGTCACAGTCACTTGAGGTTTGG	1563
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QY	1564	CCGACGACCATGATCTCCGATCTGGTTGGGCGCATCCAGCATAGGCGCATGTCAACMAA	1623
Db	314	CCGACGACCATGATCTCCGATCTGGTTGGGCGCATCCAGCATAGGCGCATGTCAACMAA	255
QY	1624	TCACCCCTGGGGCAGACACGACGAGGAGGAGACAGAGAAAAAACAACAGCATGAG	1683
Db	254	TCACCCCTGGGGCAGACACGAGGAGGAGGAGACAGAGAAAAAACAACAGCATGAG	195
QY	1684	AACACACTAATGATPAAACCATAAATATTAGCCCTCGTGTCTGTGCTTACTGGCC	1743
Db	194	AACACACTAATGATPAAACCATAAATATTAGCCCTCGTGTCTGTGCTTACTGGCC	135
QY	1744	AGGAATGATACCAATTTTTCATGTGTGACCTTGACAGCTTCTTTTGCACAAAGCAAG	1803
Db	134	AGGAATGATACCAATTTTTCATGTGTGACCTTGACAGCTTCTTTTGCACAAAGCAAG	75
QY	1804	AGAAATTAACACTGTTTCAAAACCCGGGGAGTTGGCTGTGTTAAAGAAAGACATTAAAT	1863
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QY	1864	GCCTTAGACAGTGT 1877	
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RESULT 15
US-09-867-701-1532
; Sequence 1532, Application US/09867701
; Patent No. US20020132237A1

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? GENERAL INFORMATION:
? APPLICANT: Agiate, Paul A.
? APPLICANT: Jones, Robert
? APPLICANT: Harlocker, Susan L.
? TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
? TITLE OF INVENTION: AND DIAGNOSIS OF OVARIAN CANCER
? FILE REFERENCE: 210121.497
? CURRENT APPLICATION NUMBER: US/09/867,701
? CURRENT FILING DATE: 2001-05-29
? NUMBER OF SEQ ID NOS: 10912
? SOFTWARE: PastSeq for Windows Version 4.0
? SEQ ID NO 1532
? LENGTH: 390
? TYPE: DNA
? ORGANISM: Homo sapien
? FEATURE:
? NAME/KEY: misc-feature
? LOCATION: (1)...(390)
? OTHER INFORMATION: n = A,T,C or G
US-09-867-701-1532

18.7%: Score 354; DB 10; Length 390;
Best Local Similarity 98.7%; Pred. No. 2.8e-83;
Matches 387; Conservative 0; Mismatches 2; Indels 3; Gaps 3

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QY	1608	GCCATGTCTCAACAACATCAACGCCCTGGGCGACACAGCAGAGGAGGAGACAGACAAAAG	1667
Db	120	GCCATGTCTCAACAACATCAACGCCCT -GGMAGACAGCGAGGAGGAGAGACAGACAAAAG	178
QY	1668	AAAAACACACATAGAGAACACACATTAATGATTAATAAACATCAATAATATTATTCGCCCTGT	1727
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QY	1728	TCGTGCTTACTGGCCAGGAAATGATGATCAATTTTTCAGTCTGTGACTGTGACAGCTTC -T	1788
Db	239	TCGTGCTTACTGGCCAGGAAATGATGATCAATTTTTCAGTCTGTGACTGTGACAGCTTCTT	298
QY	1787	TTTGGCCACAGCAGAGAGAGATTTTAACACTGTTTCAAAACCCGGGGAGAGTGGCTGTGTTA	1848
Db	299	TTTGGCCACAGCAGAGAGAGATTTTAACACTGTTTCAAAACCCGGGGAGAGTGGCTGTGTTA	358
QY	1847	AAGAAAGACCATTAATATGCTTTAGACAGTGTA	1878
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RESULT 15
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; Sequence 1532, Application US/09867701
; Patent No. US20020132237A1

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GenCore version 5.1.3
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OM nucleic - nucleic search, using sw model

Run on: November 7, 2002, 09:55:08 ; Search time 4250.79 seconds
(without alignments)
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Gapop 10.0, Gapext 1.0

Searched: 24791104 seqs, 12571243825 residues

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Post-processing: Minimum Match 0%

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Listing first 45 summaries

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2	1896.2	100.0	1897	1 US-09-825-294-214	Sequence 214, App
3	1896.2	100.0	1897	3 US-09-970-966-214	Sequence 214, App
4	1896.2	100.0	1897	4 US-10-212-677-214	Sequence 214, App
5	1873	98.5	1967	1 PCT-US02-29964-16	Sequence 16, App
6	1869.4	98.5	1918	1 US-09-397-022-4454	Sequence 4454, App
7	1863.2	98.2	1918	1 US-09-808-383-4454	Sequence 4454, App
8	1863.2	98.2	1925	25 US-09-652-121-7293	Sequence 7293, App
9	1863.2	98.2	1925	25 US-09-652-128-9375	Sequence 9375, App
10	1863.2	98.2	1925	25 US-09-652-917-3346	Sequence 3346, App
11	1863.2	98.2	1925	25 US-09-699-969-11085	Sequence 11085, App
12	1863.2	98.2	1925	28 US-09-710-281-4458	Sequence 4458, App
13	1863.2	98.2	1925	28 US-09-726-805-1608	Sequence 1608, App
14	1851	97.6	1917	17 US-09-371-168-7188	Sequence 7188, App
15	1851	97.6	1917	25 US-09-644-873-9077	Sequence 9077, App
16	1851	97.6	1917	25 US-09-652-109-9370	Sequence 9370, App
17	1851	97.6	1917	25 US-09-652-121-6191	Sequence 6191, App
18	1851	97.6	1917	25 US-09-652-128-7518	Sequence 7518, App
19	1851	97.6	1917	25 US-09-652-355-9112	Sequence 9112, App
20	1851	97.6	1917	25 US-09-652-914-8473	Sequence 8473, App
21	1851	97.6	1917	25 US-09-652-917-2477	Sequence 2477, App

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES


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RESULT 2
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; Sequence 214, Application US/09825294
; GENERAL INFORMATION:
; APPLICANT: Xu, Jlangchun
; APPLICANT: Stolck, John A.
; APPLICANT: Algate, Paul A.
; APPLICANT: Fling, Steven P.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
; FILE REFERENCE: 210121.484C5
; CURRENT APPLICATION NUMBER: US/09/825, 294
; NUMBER OF SEQ ID NOS: 215
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 214
; LENGTH: 1897
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc.feature
; LOCATION: (1)...(1897)
; OTHER INFORMATION: n - A,T,C or G
US-09-825-294-214

Query Match 100.0%; Score 1896.2; DB 31; Length 1897;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1897; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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D	1261	AAATCTTCTAGATTCTCTTTCGACGAGACTTGGGCGCGGAGACCGAAAGACCAAGGGGCT	1320
Q	1321	GCACAAAGCGGGGCTGTGCTGCTGTGAGTGGCATGTACGGCAGGGGCTTCTGTGT	1380
D	1321	GCACAAAGCGGGGCTGTGCTGCTGTGAGTGGCATGTACGGCAGGGGCTTCTGTGT	1380
Q	1381	TGGGCTCTGAGGAGACGGCGGCACACAGCACTGCAGAAACCCGGCGAAATCTCT	1440
D	1381	TGGGCTCTGAGGAGACGGCGGCACACAGCACTGCAGAAACCCGGCGAAATCTCT	1440
Q	1441	GCAGAGACACCGTGTACAGGAGGGGTGTATGACCGAGCTGAGGTAGAAAAACGTCTCG	1500
D	1441	GCAGAGACACCGTGTACAGGAGGGGTGTATGACCGAGCTGAGGTAGAAAAACGTCTCG	1500
Q	1501	AGAGGGGAGAGGATATAGTACGCCCGGAATGAGGACTCGTCCAGTGTGCTGGST	1560
D	1501	AGAGGGGAGAGGATATATAGCCCGGAGAGGACTCGTCCAGTGTGCTGGST	1560
Q	1561	TGGCGCGAGCCATGATTCCTCGAATCTGTGTTGGGCAATCCAGATACGGCCAATGTACAA	1620
D	1561	TGGCGCGAGCCATGATTCCTCGAATCTGTGTTGGGCAATCCAGATACGGCCAATGTACAA	1620
Q	1621	CAATCAGCCCCGGGCGACACGACGAGGAGGAGAGACAGAAAAAACAAGAT	1680
D	1621	CAATCAGCCCCGGGCGACACGACGAGGAGGAGAGACAGAAAAAACAAGAT	1680
Q	1681	GAGAACACAGTAAATGAAATAAACCAATAATTTAGCCCTCTGTTCTGTCTTACTG	1740
D	1681	GAGAACACAGTAAATGAAATAAACCAATAATTTAGCCCTCTGTTCTGTCTTACTG	1740
Q	1741	GCACGAGAAATGTACCAATTTTCAGTGTGACCTGACAGCTCTTTTGGCCACAAAGAA	1800
D	1741	GCACGAGAAATGTACCAATTTTCAGTGTGACCTGACAGCTCTTTTGGCCACAAAGAA	1800
Q	1801	GAGAGAAATTTAACACTGTTTCAAAACCCGGGGAGTGGCTGTGTTAAAGAAAGACATT	1860
D	1801	GAGAGAAATTTAACACTGTTTCAAAACCCGGGGAGTGGCTGTGTTAAAGAAAGACATT	1860
Q	1861	AATGCTTTAGACAGCTGTAATAAAAAAAAAAAAAAAAAA	1897
D	1861	AATGCTTTAGACAGCTGTAATAAAAAAAAAAAAAAAAAA	1897

RESULT 3
US-09-970-966-214

```

: GENERAL INFORMATION:
: APPLICANT: Stolk, John A.
: APPLICANT: Molesch, David Alan
: APPLICANT: Fling, Steven P.
: APPLICANT: Xu, Jiangchun
: TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
: TITLE OF INVENTION: AND DIAGNOSIS OF OVARIAN CANCER
: FILE REFERENCE: 210121.484c6
: CURRENT APPLICATION NUMBER: US/09/970,966
: CURRENT FILING DATE: 2001-10-02
: NUMBER OF SEQ ID NOS: 215
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 214
:   LENGTH: 1897
:   TYPE: DNA
: ORGANISM: Homo sapiens
: US-09-970-966-214

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query match	100.0%;	Score 1896.2;	DB 36;	Length 1897,
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Best Local Similarity 100.0%; Pred. NO. 0;
Matches 1897; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy	1	GCACACCTCGSAGGCTGTGGTCTGCTCGGCCCGGAGCGGACGCGAGCGGAGGACGACGACCG	60
Db	1	GCACACTCCGAGAGCTCTGTGCTCTCGGCCCGGAGCGGAGCGGAGGACGACGACCG	60
Oy	61	CACCGCGGAGCCCGAGGCGGGGCGATGACAGGCTCCGCGAGCGGCACTGGCGCTCTCTA	120
Db	61	CAGCGCGGAGCCCGAGGCGGGGCGATGACAGGCTCCGCGAGCGGCACTGGCGCTCTCTA	120
Oy	121	AGCTACGACCGTGTGCTTCGCGCGGCAACAGCGGGGGCCGACAGCTGTGGAGGCACAGC	180
Db	121	AGCTACGACCGTGTGCTTCGCGCGGCAACAGCGGGGGCCGACAGCTGTGGAGGCACAGC	180
Oy	181	CGCTGCAGCGGGGAGCCGACCTCCGCTCTGCTTCGCTTCGATGGCTTGGCTCTCCCG	240
Db	181	CGCTGCAGCGGGGAGCCGACCTCCGCTCTGCTTCGCTTCGATGGCTTGGCTCTCCCG	240
Oy	241	GCCCCGGGACTCGGAGAGAAATGTGGTCTTAGGCATCGCGGCACTTTTTCGGATGT	300
Db	241	GCCCCGGGACTCGGAGAGAAATGTGGTCTTAGGCATCGCGGCACTTTTTCGGATGT	300
Oy	301	CTTGCCTTCACAGGCTTTCGCTGCAATTCACAGTGTACCGGTGAAGAAATTCACAGTGA	360
Db	301	CTTGCCTTCACAGGCTTTCGCTGCAATTCACAGTGTACCGGTGAAGAAATTCACAGTGA	360
Oy	361	CAACGACTGCTCCTCCCCGAGTTCAATTGTGAATTGCACGGTGAACGTTCAAGACATGTG	420
Db	361	CAACGACTGCTCCTCCCCGAGTTCAATTGTGAATTGCACGGTGAACGTTCAAGACATGTG	420
Oy	421	TCGAAAGAAGTATGGAGCAAGATCGCGGATTCATGTACCCAGTCTCTGATCATC	480
Db	421	TCGAAAGAAGTATGGAGCAAGATCGCGGATTCATGTACCCAGTCTCTGATCATC	480
Oy	481	AGCGGCGCTGTCTCATGCGCTCTTCGCGGGTACCAAGTCTTCTGCTCCCGAGGAAACTGTAA	540
Db	481	AGCGGCGCTGTCTCATGCGCTCTTCGCGGGTACCAAGTCTTCTGCTCCCGAGGAAACTGTAA	540
Oy	541	CTCAGTTGGATCAGCGTGTCAACACCCCTCTTGTACGGGGCAAGGCCCAAGAAAG	600
Db	541	CTCAGTTGGATCAGCGTGTCAACACCCCTCTTGTACGGGGCAAGGCCCAAGAAAG	600
Oy	601	GGAAGATTGCTCGGCGCTCAAGGCCAGGGCTCCGACACACATCTGTTCCTCAATT	660
Db	601	GGAAGATTGCTCGGCGCTCAAGGCCAGGGCTCCGACACACATCTGTTCCTCAATT	660
Oy	661	AGCCCTCTTCGCGCACACTGTGAAGCTGAAGAGATGCCACCCCTCTGCAATTGTTC	720
Db	661	AGCCCTCTTCGCGCACACTGTGAAGCTGAAGAGATGCCACCCCTCTGCAATTGTTC	720
Oy	721	TTTCAGCCCTCGGCCCAACCCCAACCTCCCTGAGTGAATTTCTTGTGGTGTCCTTTT	780
Db	721	TTTCAGCCCTCGGCCCAACCCCAACCTCCCTGAGTGAATTTCTTGTGGTGTCCTTTT	780
Oy	781	ATTCTGGGTAGGAGGCGGGAGTCCGATGCTCTTTGTTCCTGTGCAATAATATGAAGAG	840
Db	781	ATTCTGGGTAGGAGGCGGGAGTCCGATGCTCTTTGTTCCTGTGCAATAATATGAAGAG	840
Oy	841	CTCGGTAAAGCATTCGTAATAAATTTAGCCTGACTGAATTTTCAATATGTACTGAAGA	900
Db	841	CTCGGTAAAGCATTCGTAATAAATTTAGCCTGACTGAATTTTCAATATGTACTGAAGA	900
Oy	901	AGGAGGTGTGAAGTAAAGTTACCCCATATGTCTGTGAACCGGAGTCAAGGCCAGGCTGGC	960
Db	901	AGGAGGTGTGAAGTAAAGTTACCCCATATGTCTGTGAACCGGAGTCAAGGCCAGGCTGGC	960
Oy	961	AGAGCTGCTCTTGAAGTCACTGAGGTGGGATCGCTTTTGTGAAGCCTCCAGTGTCTC	1020
Db	961	AGAGCTGCTCTTGAAGTCACTGAGGTGGGATCGCTTTTGTGAAGCCTCCAGTGTCTC	1020
Oy	1021	CATTTCATCCCTGATGGGGCATAGTTTGAGACTGACAGTGAAGTGAAGTCTTCTTCTAG	1080

Db	1021	CATTCATCCCTGATG6GGGGCATAGTTTGAGACTGCAAGTGAAGTGAAGTGTTCCTTAC	1080
Qy	1081	GGCTGGAGGGCCAGTTCGCCACTCAAGGCTCCCTCGCTTGACATTCAACTTCATGCTCCT	1140
Db	1081	GCGTGGAGGGCCAGTTCGCCACTCAAGGCTCCCTCGCTTGACATTCAAACTTCATGCTCCT	1140
Qy	1141	GAAACCATCTCTCGCAGCAGAAATTTGGCTGTTCGCGCTGAGTTGGGCTGTAGTACT	1200
Db	1141	GAAACCATCTCTGCAAGCAGAAATTTGGCTGTTCGCGCTGAGTTGGGCTGTAGTACT	1200
Qy	1201	CGAGACTCAATGACTGTGGACTTAACTAGCTGGGGCTCGGCTCTGCTGTGAAAAGCTTAA	1260
Db	1201	CGAGACTCAATGACTGTGGACTTAACTAGCTGGGGCTCGGCTCTGCTGTGAAAAGCTTAA	1260
Qy	1261	AAATCTTCACATTCCTCCTTGCAAGAGACTGGCGGGGACGGGAAGAGAAAGGGGGCT	1320
Db	1261	AAATCTTCACATTCCTCCTTGCAAGAGACTGGCGGGGACGGGAAGAGAAAGGGGGCT	1320
Qy	1321	GCACAAAGCGGGCGCTGTGCGTGGTGGAGTGGCATGTACGCCAGCGGCTTCGTGGT	1380
Db	1321	GCACAAAGCGGGCGCTGTGCGTGGTGGAGTGGCATGTACGCCAGCGGCTTCGTGGT	1380
Qy	1381	TGGCGTGTGCAAGCGCAGCGGCGGACACAGACCTGTGCAGAACACCCGGCGAACTGCT	1440
Db	1381	TGGCGTGTGCAAGCGCAGCGGCGGACACAGACCTGTGCAGAACACCCGGCGAACTGCT	1440
Qy	1441	GGGAGGACCCCTGTACAGAGAGCGGGTTATGACCCAGCTGAGAGTAAAAAGCTCCG	1500
Db	1441	GGGAGGACCCCTGTACAGAGAGCGGGTTATGACCCAGCTGAGAGTAAAAAGCTCCG	1500
Qy	1501	AGAGGGGAGAGAGATCATGTACGCCCGGAAAGTAAAGTAAAGTGTGGGTT	1560
Db	1501	AGAGGGGAGAGAGATCATGTACGCCCGGAAAGTAAAGTAAAGTGTGGGTT	1560
Qy	1561	TGGCGGACCCATGTATCCCGAATGTGGTGTGGGCAATCAAGCATACGGCCCAATGTCAA	1620
Db	1561	TGGCGGACCCATGTATCCCGAATGTGGTGTGGGCAATCAAGCATACGGCCCAATGTCAA	1620
Qy	1621	CAATCAGCCCTGGGAGACAGCAGCGAGGAGGAGAGACAGAAAAAGAAACACACAT	1680
Db	1621	CAATCAGCCCTGGGAGACAGCAGCGAGGAGGAGAGACAGAAAAAGAAACACACAT	1680
Qy	1681	GAGAACACAGTAAATGAATAAAAACCTAAATATTAGCCCTCTGTCTGTGCTTACTG	1740
Db	1681	GAGAACACAGTAAATGAATAAAAACCTAAATATTAGCCCTCTGTCTGTGCTTACTG	1740
Qy	1741	GCCAGAAATGGTACCATTCTTTCAGTGTGGACTTGACAGCTTCTTTTCCCAACAA	1800
Db	1741	GCCAGAAATGGTACCATTCTTTCAGTGTGGACTTGACAGCTTCTTTTCCCAACAA	1800
Qy	1801	GAGGAATTTAACACTGTTCACAAACCCGGGGAGTGGCTGTGTAAAGAACCATTA	1860
Db	1801	GAGGAATTTAACACTGTTCACAAACCCGGGGAGTGGCTGTGTAAAGAACCATTA	1860
Qy	1861	AATGCTTAGACAGTGTAAAAAAGAAAAAAGAAAAA 1897	
Db	1861	AATGCTTAGACAGTGTAAAAAAGAAAAAAGAAAAA 1897	

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RESULT 4
US-10-212-677-214
: Sequence 214, Application US/10212677
: GENERAL INFORMATION:
: APPLICANT: Chenault, Ruth A.
: APPLICANT: Xu, Jiangchun
: APPLICANT: Fanger, Gary R.
: APPLICANT: Harlocker, Susan L.
: APPLICANT: McNeill, Patricia D.
: TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
: OF OVARIAN CANCER
: FILE REFERENCE: 210121.484C/7
: CURRENT APPLICATION NUMBER: US/10/212.677
: CURRENT FILING DATE: 2002-08-02

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; NUMBER OF SEQ ID NOS: 288
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 214
; LENGTH: 1697
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-10-212-677-214

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Query Match	100.0%;	Score 1896.2;	DB 42;	Length 1897;
Best Local Similarity	100.0%;	Pred. NC. 0;		
Matches 1897: Conservative	0;	Mismatches	0;	Indels 0; Gaps 0;

QY	1	GCGAATCTCCGAGGCTGTGTGCTCGGCGCGGAGACGAGCGGAGAGACGACCG	60
Db	1	GCGAATCTCCGAGGCTGTGTGCTCGGCGCGGAGACGAGCGGAGAGACGAGACCG	60
QY	61	CAGCGGAGACCCGACGCGGGGCGATGAGGCTCCGCGAGCGGACCTGGGGTCTCTA	120
Db	61	CAGCGGAGAGCCGACGCGGGGCGATGAGGCTCCGCGAGCGGACCTGGGGTCTCTA	120
QY	121	AGCTACGACCGTCTCTCCGGGAGAGACGCGGGGCCACGACCTTCGCGAGGACAGC	180
Db	121	AGCTACGACCGTCTCTCCGGGAGAGACGCGGGGCCACGACCTTCGCGAGGACAGC	180
QY	181	CGCTGACGCGGGGACGCTCCGCTGCTGACCTCTGTGATGCGCTTGGCCCTCCCG	240
Db	181	CGCTGACGCGGGGACGCTCCGCTGCTGACCTCTGTGATGCGCTTGGCCCTCCCG	240
QY	241	GCCCCGGGACCTCGGGAGAAATGGTGGTCTMGAGATGCGGCAACTTTTGGGATTTGT	300
Db	241	GCCCCGGGACCTCGGGAGAAATGGTGGTCTMGAGATGCGGCAACTTTTGGGATTTGT	300
QY	301	CTTGCTTCCAGGCTTTTGCGCTGCAAAATCCAGTGTACAGTGTAAATAATCCAGCTGAA	360
Db	301	CTTGCTTCCAGGCTTTTGCGCTGCAAAATCCAGTGTACAGTGTAAATAATCCAGCTGAA	360
QY	361	CAAGACTGCTCTCCCCCGAGTTCAATTGTGAATTGCAAGGTGAAGCTTCAAGACATGTG	420
Db	361	CAAGACTGCTCTCCCCCGAGTTCAATTGTGAATTGCAAGGTGAAGCTTCAAGACATGTG	420
QY	421	TCAGAAAGAAATGTATGAGAGCAAAATGCGGGATATGTACGCAAGTCTGTGATATC	480
Db	421	TCAGAAAGAAATGTATGAGAGCAAAATGCGGGATATGTACGCGAAGTCTGTGATATC	480
QY	481	AGCGGCTGTCTATTCGCTCTGCGGGATACAGTCTTCTGCTCCCGAGGAATGTAA	540
Db	481	AGCGGCTGTCTATTCGCTCTGCGGGATACAGTCTTCTGCTCCCGAGGAATGTAA	540
QY	541	CTCAGTTTGATCGATGCTGCTGACACACCCCTTTGTAAGGGGCAAGGCCAGAGAAAG	600
Db	541	CTCAGTTTGATCGATGCTGCTGACACACCCCTTTGTAAGGGGCAAGGCCAGAGAAAG	600
QY	601	GCGAAGTTCTGCTCGGCGCTCAGGCGAGGCTTCGACACCAACCATCTGTTCTCAAAAT	660
Db	601	GCGAAGTTCTGCTCGGCGCTCAGGCGAGGCTTCGACACCAACCATCTGTTCTCAAAAT	660
QY	661	AGCCCTCTTCTCGGCAACGTGTAACTGAAGAAATGCCACCCCTCTGCAATTGTTC	720
Db	661	AGCCCTCTTCTCGGCAACGTGTAACTGAAGAAATGCCACCCCTCTGCAATTGTTC	720
QY	721	TTCCAGCCCTCGCCCCCAACCCCCACGCTCCGTAAGAGATTTCTTGGGTGACTTTT	780
Db	721	TTCCAGCCCTCGCCCCCAACCCCCACGCTCCGTAAGAGATTTCTTGGGTGACTTTT	780
QY	781	ATTCTGGGTAGGAGCGGGAGTCCGTTCTCTTTGTCTCTGTGCAATATGAAAGAG	840
Db	781	ATTCTGGGTAGGAGCGGGAGTCCGTTCTCTTTGTCTCTGTGCAATATGAAAGAG	840
QY	841	CTCGGTAAACCATTTCAATTAATATTCAGCTGTGACTGAATTTTCAGTATGTACTTAAAGGA	9000
Db	841	CTCGGTAAACCATTTCTAATTAATATTCAGCTGTGACTGAATTTTCAGTATGTACTTAAAGGA	9000
QY	901	AGGAGGTGAGTAAGTTACCCCTCATGCTGTGTAAACCGGAGTCAAGGCCAGGCTGCC	9600


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Db 319 GCCCGGAGCTCCGGAGAAATGTGGTCTTGAAGCATCGCGCAACTTTTTCGGATTGTT 378
QY 301 CTTCCTTCAGAGCTTTGGGCTGCAAAATCCAGTGTCTACAGTGTGAAGAAATTCAGGCGAA 360
Db 379 CTTCCTTCAGAGCTTTGGGCTGCAAAATCCAGTGTCTACAGTGTGAAGAAATTCAGGCTGAA 438
QY 361 CAAGACCTGCTCTCCCGAGTTCATTTGTAATTCAGGCGTGAACGTTCAACACATGTTG 420
Db 439 CAAGACCTGCTCTCCCGAGTTCATTTGTAATTCAGGCGTGAACGTTCAACACATGTTG 498
QY 421 TCAGAAAGAGTGTAGAGCAAAAGTGGGGGATCATGTACCCCAATCTCTGTGATCATC 460
Db 499 TCAGAAAGAGTGTAGAGCAAAAGTGGGGGATCATGTACCCCAATCTCTGTGATCATC 558
QY 481 AGCGGCTGTCTCATCGGCTCTGCCGGGTACCAATCTCTGTGATCATC 540
Db 559 AGCGGCTGTCTCATCGGCTCTGCCGGGTACCAATCTCTGTGATCATC 618
QY 541 CTCAGTTTGCATTCAGTCTCTGCAACACCCCTTTTGAAGGCGCCCAAGGCGCAAGAAAG 600
Db 619 CTCAGTTTGCATTCAGTCTCTGCAACACCCCTTTTGAAGGCGCCCAAGGCGCAAGAAAG 678
QY 601 GGAAGTCTCTGCTCTGCGGCTCTGAGGCGGCGGCTCCGACACACATCTCTCTCAAAAT 660
Db 679 GGAAGTCTCTGCTCTGCGGCTCTGAGGCGGCGGCTCCGACACACATCTCTCTCAAAAT 738
QY 661 AGCCCTCTCTGCGCACACTGCTGAAGCTGAAGAGATGCGACCCCTCTGATGTTG 720
Db 739 AGCCCTCTCTGCGCACACTGCTGAAGCTGAAGAGATGCGACCCCTCTGATGTTG 798
QY 721 TTCCAGGCTCTGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 780
Db 799 TTCCAGGCTCTGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 858
QY 781 ATTCTGGGTAGGAGCGGAGTCCGCTCTCTTTGTTGCTCTGCTGCAAAATTAAGAAAG 840
Db 859 ATTCTGGGTAGGAGCGGAGTCCGCTCTCTTTGTTGCTCTGCTGCAAAATTAAGAAAG 918
QY 841 CTGCGTAAAGCATTTCTGAATTAATTCAGCTGATGAATTTTCAATGATCTTGAAGGA 900
Db 919 CTGCGTAAAGCATTTCTGAATTAATTCAGCTGATGAATTTTCAATGATCTTGAAGGA 978
QY 901 AGGAGTGTAGTGAAGTTCACCCCATGTCGTGTACCGGAGTCAAGGCGGCGGCGGCGG 960
Db 979 AGGAGTGTAGTGAAGTTCACCCCATGTCGTGTACCGGAGTCAAGGCGGCGGCGGCGG 1038
QY 961 AGAGTGTGTCTTGAAGTCACTGAGGTGGCATCTGCTTTTGAAGGCGTCCAGTGTG 1020
Db 1039 AGAGTGTGTCTTGAAGTCACTGAGGTGGCATCTGCTTTTGAAGGCGTCCAGTGTG 1098
QY 1021 CATTCATCTCTGATGGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 1080
Db 1099 CATTCATCTCTGATGGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 1158
QY 1081 GGGTGTAGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 1140
Db 1159 GGGTGTAGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 1218
QY 1141 GAAACCATTTCTGCGACGCAAAATTTGCTGCGGCGGCGGCGGCGGCGGCGGCGGCGG 1200
Db 1219 GAAACCATTTCTGCGACGCAAAATTTGCTGCGGCGGCGGCGGCGGCGGCGGCGGCGG 1278
QY 1201 CGAGACTCATGACTGGAGCTTACAGTGGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 1260
Db 1279 CGAGACTCATGACTGGAGCTTACAGTGGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 1338
QY 1261 AAATCTTTCAGTTCCTTTCGAGAGACTTGGCGCGGCGGCGGCGGCGGCGGCGGCGG 1320
Db 1339 AAATCTTTCAGTTCCTTTCGAGAGACTTGGCGCGGCGGCGGCGGCGGCGGCGGCGG 1398
QY 1321 GCACAAAGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 1380
Db 1399 GCACAAAGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 1458

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QY 1381 TGGCGTGTCTGACGACGACGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 1440
Db 1459 TGGCGTGTCTGACGACGACGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 1518
QY 1441 GCGAGGACACCGGTGTACAGGAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 1500
Db 1519 GCGAGGACACCGGTGTACAGGAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 1578
QY 1501 AGAAGGAGGAGGATCATGTGACGCGCGGGAAGTAGGACCTGCTCCAGTCTGCTGGGTT 1560
Db 1579 AGAAGGAGGAGGATCATGTGACGCGCGGGAAGTAGGACCTGCTCCAGTCTGCTGGGTT 1638
QY 1561 TGGCGGAGGCGGATGATCTCTCGGAATCTGTTGGGCGATCAGATATACGCGCAATGTCACA 1620
Db 1639 TGGCGGAGGCGGATGATCTCTCGGAATCTGTTGGGCGATCAGATATACGCGCAATGTCACA 1698
QY 1621 CAATCAGCCCTGGGCGAGACGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAT 1680
Db 1699 CAATCAGCCCTGGGCGAGACGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAT 1758
QY 1681 GAGACACAGTAAATGAATTAATAACCAATTAATTAATTAATTAATTAATTAATTAATTA 1740
Db 1759 GAGACACAGTAAATGAATTAATAACCAATTAATTAATTAATTAATTAATTAATTAATTA 1818
QY 1741 GCCAGAAATGTACCAATTTTTCAGTGTGAGCTTGACGCTTCTTTTCCACAGCA 1800
Db 1819 GCCAGAAATGTACCAATTTTTCAGTGTGAGCTTGACGCTTCTTTTCCACAGCA 1878
QY 1801 GAGAAATTTAACAATTTTTCACACCGGCGGAGTGTGCTGTGAAGAAAGACATTA 1860
Db 1879 GAGAAATTTAACAATTTTTCACACCGGCGGAGTGTGCTGTGAAGAAAGACATTA 1938
QY 1861 AATGCTTTAACAATTTTTCACACCGGCGGAGTGTGCTGTGAAGAAAGACATTA 1889
Db 1939 AATGCTTTAACAATTTTTCACACCGGCGGAGTGTGCTGTGAAGAAAGACATTA 1967

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RESULT 6
US-09-397-022-4454
; Sequence 4454, Application US/09397022
; GENERAL INFORMATION:
; APPLICANT: Gearing, David P.
; APPLICANT: Holzman, Douglas A.
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES DERIVED FROM A
; FILE REFERENCE: M198-46PM
; CURRENT APPLICATION NUMBER: US/09/397, 022
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100, 465
; PRIOR FILING DATE: 1998-09-15
; PRIOR APPLICATION NUMBER: 60/106, 443
; PRIOR FILING DATE: 1998-10-30
; PRIOR APPLICATION NUMBER: 60/107, 257
; PRIOR FILING DATE: 1998-11-05
; PRIOR APPLICATION NUMBER: 60/126, 906
; PRIOR FILING DATE: 1999-03-30
; PRIOR APPLICATION NUMBER: 60/132, 099
; PRIOR FILING DATE: 1999-04-30
; NUMBER OF SEQ ID NOS: 5775
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 4454
; LENGTH: 1918
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-397-022-4454

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Query Match 98.5%; Score 1869.4; DB 17; Length 1918;
Best Local Similarity 99.7%; Pred. No. 0;
Matches 1881; Conservative 2; Mismatches 3; Indels 1; Gaps 1;
QY 1 GCCAATCTCGAGAGCTGTGCTGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 1

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Db 18 GCCAACTCCGAGGCGC-GGTGCTCGGCGCCGGAGACCGGAGGAGGAGAGACGAGACGCC 76
Oy 61 CAGCCGGGAGGCCGAGCGGGGATGAGGCTCCGAGCGGACCTGCGGCTCTTA 120
Db 77 CAGCGGGAGGCCGAGCGGGGATGAGGCTCCGAGCGGACCGGCGGCTCTTA 136
Oy 121 AGCTACGACGCTCTCTCCGGGAGAGCGCGGGGCCACGACGCTCGGGAGCGACAGC 180
Db 137 AGCTACGACGCTCTCTCCGGGAGAGCGCGGGGCCACGACGCTCGGGAGCGACAGC 196
Oy 181 CGCTGACGCGGGGAGCGCTCCGCTGCTGCTCTCTGATGGCTTGGCTCTCCG 240
Db 197 CGCTGACGCGGGGAGCGCTCCGCTGCTGCTCTCTGATGGCTTGGCTCTCCG 256
Oy 241 GCGCGGGAGCTCCGGGAGATGGGCTCTAGGCTCGCGGACCTTTTGGGATTTGT 300
Db 257 GCGCGGGAGCTCCGGGAGATGGGCTCTAGGCTCGCGGACCTTTTGGGATTTGT 316
Oy 301 CTGCTTCCAGGCTTGGGCTGGCAAAATCGATGCTAGCAGTGAAGAAATTCACATGAA 360
Db 317 CTGCTTCCAGGCTTGGGCTGGCAAAATCGATGCTAGCAGTGAAGAAATTCACATGAA 376
Oy 361 CAAGACGCTCTCTCCCGAGTTCTATTGTGAATTCAGCGGTGAAGCTTCAAGACATGTG 420
Db 377 CAAGACGCTCTCTCCCGAGTTCTATTGTGAATTCAGCGGTGAAGCTTCAAGACATGTG 436
Oy 421 TCAGAAAGATGATGAGCAAAAGTCCGGGATCATGTAACGCAAGTCCGTCGATCATC 480
Db 437 TCAGAAAGATGATGAGCAAAAGTCCGGGATCATGTAACGCAAGTCCGTCGATCATC 496
Oy 481 AGCGGCTGTCTCATGCGCTCTGCGGGTACAGTCTTGTGCTCCCGAGGAACTGAA 540
Db 497 AGCGGCTGTCTCATGCGCTCTGCGGGTACAGTCTTGTGCTCCCGAGGAACTGAA 556
Oy 541 CTGAGTTTGCATCAGCTGCTGCAACACCTCTTTTGAACGGGCCCAAGGCCCAAGAAAG 600
Db 557 CTGAGTTTGCATCAGCTGCTGCAACACCTCTTTTGAACGGGCCCAAGGCCCAAGAAAG 616
Oy 601 GGGAGTTTGTGCTGGGCTCTGAGGCAAGGCTCCGACACCATCTGTTCTCAAT 660
Db 617 GGGAGTTTGTGCTGGGCTCTGAGGCAAGGCTCCGACACCATCTGTTCTCAAT 676
Oy 661 AGCCCTTCTCTGCGACACTGCTGAAGCTGAAGAGATGCCAACCCTCTGCTCATTTGTC 720
Db 677 AGCCCTTCTCTGCGACACTGCTGAAGCTGAAGAGATGCCAACCCTCTGCTCATTTGTC 736
Oy 721 TTCCAGACCTCGCCGCCCAACCCGCCACCTCCCTGAGTGAATTTCTTCTGGTCTCTTT 780
Db 737 TTCCAGACCTCGCCGCCCAACCCGCCACCTCCCTGAGTGAATTTCTTCTGGTCTCTTT 796
Oy 781 ATTCTGGGTAGGAGGAGGAGTCCGTTCTCTTTTGTCTGTCGTAATAATGAAGAG 840
Db 797 ATTCTGGGTAGGAGGAGGAGTCCGTTCTCTTTTGTCTGTCGTAATAATGAAGAG 856
Oy 841 CTCGGTAAGCATTTCTGAATTAATTCAGCTGATGATTTCTGATGAGGA 900
Db 857 CTCGGTAAGCATTTCTGAATTAATTCAGCTGATGATTTCTGATGAGGA 916
Oy 901 AGGAGTGAAGTGAAGTTCACCCCATCTCTGTGAACCGGAGCAAGGCGGCTGGC 960
Db 917 AGGAGTGAAGTGAAGTTCACCCCATCTCTGTGAACCGGAGCAAGGCGGCTGGC 976
Oy 961 AGAGTGMTCCTTGAAGTCACTGAGTGGGCTGCTCTTTTGTAAAGCTCCAGTGTG 1020
Db 977 AGAGTGMTCCTTGAAGTCACTGAGTGGGCTGCTCTTTTGTAAAGCTCCAGTGTG 1036
Oy 1021 CATTCATCCCTGATGGGGCATAGTTTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 1080
Db 1037 CATTCATCCCTGATGGGGCATAGTTTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 1096
Oy 1081 GGTGAGAGGCGGATTCACACTGAAGGCTCCCTGCTTGAAGTGAAGTGAAGTGAAGTGAAG 1140
Db 1097 GGTGAGAGGCGGATTCACACTGAAGGCTCCCTGCTTGAAGTGAAGTGAAGTGAAGTGAAG 1156

Oy 1141 GAAACCATTCCTGACACAGAAATTTGGCTGTTGCGCCTGATGTTGGCTCTAGTACT 1200
Db 1157 GAAACCATTCCTGACACAGAAATTTGGCTGTTGCGCCTGATGTTGGCTCTAGTACT 1216
Oy 1201 CGAGACTCAATGACTGGGACTTGAAGTGGGCTCGGCTCTGTAAGTCTTAAGA 1260
Db 1217 CGAGACTCAATGACTGGGACTTGAAGTGGGCTCGGCTCTGTAAGTCTTAAGA 1276
Oy 1261 AAATCTTCTGACTTCTCTTTCAGAGGACTGGCGCGGGAGCGGAGCAAGCGGCGCT 1320
Db 1277 AAATCTTCTGACTTCTCTTTCAGAGGACTGGCGCGGGAGCGGAGCAAGCGGCGCT 1336
Oy 1321 GCACAAAGCGGCGCTGTCGCTGCTGAGTGGAGTGGCATGACGCGGAGCGCTCTGCTGT 1380
Db 1337 GCACAAAGCGGCGCTGTCGCTGCTGAGTGGAGTGGCATGACGCGGAGCGCTCTGCTGT 1396
Oy 1381 TGGCTGCTGACGAGCAGCGGCGGAGCAGACAGCAGCTGACAGCAACCGCGGAACTGCT 1440
Db 1397 TGGCTGCTGACGAGCAGCGGCGGAGCAGACAGCAGCTGACAGCAACCGCGGAACTGCT 1456
Oy 1441 GCGAGGACACGCTGTACAGGAGCGGGTGTGATGACGAGCTGAGTGAAGAAAGCTCTCG 1500
Db 1457 GCGAGGACACGCTGTACAGGAGCGGGTGTGATGACGAGCTGAGTGAAGAAAGCTCTCG 1516
Oy 1501 AGAAGGGAGAGATCATGTACGCCCGGAAATGAGACCTGCTCAAGTCTGCTTGGCTT 1560
Db 1517 AGAAGGGAGAGATCATGTACGCCCGGAAATGAGACCTGCTCAAGTCTGCTTGGCTT 1576
Oy 1561 TGGCGGACGCTGATCTCTCCGAATCTGTTGGGATCCAGATTCAGGCAATGTCACAA 1620
Db 1577 TGGCGGACGCTGATCTCTCCGAATCTGTTGGGATCCAGATTCAGGCAATGTCACAA 1636
Oy 1621 CAATCAGCCCTGGGAGACAGCAGAGAGAGAGACAGAGAGAGAGAGAGAGAGAGAGAGAT 1680
Db 1637 CAATCAGCCCTGGGAGACAGCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAT 1696
Oy 1681 GAGAACACAGTAAATGAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1740
Db 1697 GAGAACACAGTAAATGAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1756
Oy 1741 GCGAGAAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1800
Db 1757 GCGAGAAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1816
Oy 1801 GAGAGAAATTAACACTGTTTCAAAACCCGGGAGTGGCTGTTTAAAGAAAGACCATTA 1860
Db 1817 GAGAGAAATTAACACTGTTTCAAAACCCGGGAGTGGCTGTTTAAAGAAAGACCATTA 1876
Oy 1861 AATGCTTTAGACAGTGTAAAAAAA 1887
Db 1877 AATGCTTTAGACAGTGTAAAAAAA 1903

RESULT 7
US-09-808-383-4454
; Sequence 4454, Application US/09808383
; GENERAL INFORMATION:
; APPLICANT: Geating, David P.
; APPLICANT: Holtzman, Douglas A.
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES DERIVED FROM A
; FILE REFERENCE: 1600,1046-002
; CURRENT APPLICATION NUMBER: US/09/808,383
; PRIOR FILING DATE: 2001-03-13
; PRIOR APPLICATION NUMBER: US 09/397,022
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: US 60/100,465
; PRIOR FILING DATE: 1998-09-15
; PRIOR APPLICATION NUMBER: US 60/106,443
; PRIOR FILING DATE: 1998-10-30
; PRIOR APPLICATION NUMBER: US 60/107,257
; PRIOR FILING DATE: 1998-11-15


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QY 1861 AATGCTTTAGACAGTGTAAAAA 1884
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Db 46 AATGCTTTAGACAGTGTATTTAA 23

RESULT 9
US-09-652-128-9375/c
; Sequence 9375, Application US/09652128
; GENERAL INFORMATION:
; APPLICANT: Shvjan, Andrew W.
; TITLE OF INVENTION: NOVEL NUCLEIC ACID MOLECULES AND USES
; FILE REFERENCE: 1600,1171-001
; CURRENT APPLICATION NUMBER: US/09/652,128
; PRIOR FILING DATE: 2000-08-30
; PRIOR APPLICATION NUMBER: 60/151,133
; NUMBER OF SEQ ID NOS: 10265
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 9375
; LENGTH: 1925
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-652-128-9375

Query Match      98.2%  Score 1863.2;  DB 25;  Length 1925;
Best Local Similarity 99.6%;  Pred. No. 0;
Matches 1876;  Conservative 2;  Mismatches 5;  Indels 1;  Gaps 1;
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Db 1306 GGGAAATTCTGCTCGGGCCCTCAGGCCACTCCGACACACATCTCTTCTCAAAAT 1247
QY 661 AGCCCTCTTTCGGACACTGCTGAAGATGCCACCCCTCTGCAATTTGTC 720
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Db 1246 AGCCCTCTTTCGGACACTGCTGAAGATGCCACCCCTCTGCAATTTGTC 1187
QY 721 TTCCAGCCCTCGCCCCCAACCCCTCCCTAGTGAATTTCTTCTGCGGTCTCTTT 780
    |||||
Db 1186 TTCCAGCCCTCGCCCCCAACCCCTCCCTAGTGAATTTCTTCTGCGGTCTCTTT 1127
QY 781 ATTCTGGGTAGGAGAGCGGAGTCCGTCTCTTTGTTCTGTGCAATATATGAAG 840
    |||||
Db 1126 ATTCTGGGTAGGAGAGCGGAGTCCGTCTCTTTGTTCTGTGCAATATATGAAG 1067
QY 841 CTGCGTAAGCAATTTCTGAATTAATTCAGTCATGTAATTTTCAATATGATGAAGA 900
    |||||
Db 1066 CTGCGTAAGCAATTTCTGAATTAATTCAGTCATGTAATTTTCAATATGATGAAGA 1007
QY 901 AGGAGGTGAGTGAAGTTACCCCCCATGTCGTGTAACCGGACTCAAGGCCAGCTGGC 960
    |||||
Db 1006 AGGAGGTGAGTGAAGTTACCCCCCATGTCGTGTAACCGGACTCAAGGCCAGCTGGC 947
QY 961 AGAGTCMTCTCTTAGAAGTCACTGAGGTGGGCATCTGCTTTTGTAAAGCTCCAGTGT 1020
    |||||
Db 946 AGAGTCAGTCTTAGAAGTCACTGAGGTGGGCATCTGCTTTTGTAAAGCTCCAGTGT 887
QY 1021 CATTCATCTCTGATGAGGAGGATGTTGAGACTGCAAGAGTGAAGTGAAGTCTTCTTAG 1080
    |||||
Db 886 CATTCATCTCTGATGAGGAGGATGTTGAGACTGCAAGAGTGAAGTGAAGTCTTCTTAG 827
QY 1081 GCGTGAAGGAGGAGTTCCTCCACTCAAGGCTCCCTGCTTGAATCAATCAATCTCTCT 1140
    |||||
Db 826 GCGTGAAGGAGGAGTTCCTCCACTCAAGGCTCCCTGCTTGAATCAATCAATCTCTCT 767
QY 1141 GAAACCAATTTCTGACAGCAAAATTTGGCTGTTTCCGCGCTGAGTGGGCTCTAGTACT 1200
    |||||
Db 766 GAAACCAATTTCTGACAGCAAAATTTGGCTGTTTCCGCGCTGAGTGGGCTCTAGTACT 707
QY 1201 CGAGACTCAATGACTGGGACTTGAAGTGGGCTCTGCGCTGCTGTAAGAGTCTTAAGA 1260
    |||||
Db 706 CGAGACTCAATGACTGGGACTTGAAGTGGGCTCTGCGCTGCTGTAAGAGTCTTAAGA 647
QY 1261 AATATCTTCAGTTCTTCCTTTCAGAGAGACTGGGCGCGGAGCGCAAGAGCAAGCGGCGCT 1320
    |||||
Db 646 AATATCTTCAGTTCTTCCTTTCAGAGAGACTGGGCGCGGAGCGCAAGAGCAAGCGGCGCT 587
QY 1321 GCACAAAGCGGGGCGCTGCTGCTGCTGAGTGGCAGTACGCGCAGGCGCTTCTGCTGT 1380
    |||||
Db 586 GCACAAAGCGGGGCGCTGCTGCTGCTGAGTGGCAGTACGCGCAGGCGCTTCTGCTGT 527
QY 1381 TGGCGGTGTCAGAGCGACAGGCGGCGACAGCAACCTGCAAGAACCCCGCGGAATGCT 1440
    |||||
Db 526 TGGCGGTGTCAGAGCGACAGGCGGCGACAGCAACCTGCAAGAACCCCGCGGAATGCT 467
QY 1441 GCGAGGACACCGTGTACAGAGCGGGTTGATGACCGAGCTGAGAGTAAAGAAACCTCTCCG 1500
    |||||
Db 466 GCGAGGACACCGTGTACAGAGCGGGTTGATGACCGAGCTGAGAGTAAAGAAACCTCTCCG 407
QY 1501 AGAAGGGAGAGGAGTATGATGACCGCGGAGTGAAGCACTGCTCAGTCTGCTTGGGTT 1560
    |||||
Db 406 AGAAGGGAGAGGAGTATGATGACCGCGGAGTGAAGCACTGCTCAGTCTGCTTGGGTT 347
QY 1561 TGGCGGACCATGATCTCTCCGAATCTGGTTGGGCATCCAGCAATAGGCCCAATGTCACAA 1620
    |||||
Db 346 TGGCGGACCATGATCTCTCCGAATCTGGTTGGGCATCCAGCAATAGGCCCAATGTCACAA 287
QY 1621 CAATCAGCCCTGGGCGAGACAGGAGGAGAGAGACAGAGAAAAAGAAAAACACACAT 1680
    |||||
Db 286 CAATCAGCCCTGGGCGAGACAGGAGGAGAGAGAGAGAAAAAGAAAAACACACAT 227
QY 1681 GAGAACACAGTAAATGAATAAAAACCTTAAATATTAAAGCCCTCTGCTGCTTAACTG 1740
    |||||
Db 226 GAGAACACAGTAAATGAATAAAAACCTTAAATATTAAAGCCCTCTGCTGCTTAACTG 167
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Db 346 TGCCCGCAGCCATGATCTCCGAAATCTGTTGGCATCCAGCATACGCCAATGTCACAA 287
 QY 1621 CAATCAGCCCTGGCAGACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAT 1680
 Db 286 CAATCAGCCCTGGCAGACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAT 227
 QY 1681 GAGAACACAGTAAATGAATAAACCATAAATATTTAGCCCTCTGTTCTGCTTACTG 1740
 Db 226 GAGAACACAGTAAATGAATAAACCATAAATATTTAGCCCTCTGTTCTGCTTACTG 167
 QY 1741 GCCAGGAATGTCACATTTTTCAGTGTGACCTTGTGACAGTCTTTTGGCAGAGAA 1800
 Db 166 GCCAGGAATGTCACATTTTTCAGTGTGACCTTGTGACAGTCTTTTGGCAGAGAA 107
 QY 1801 GAGAGATTTTAACTGTTTCAACCCCGGGAGTTGGCTGTGTTAAGAAAGACCATTA 1860
 Db 106 GAGAGATTTTAACTGTTTCAACCCCGGGAGTTGGCTGTGTTAAGAAAGACCATTA 47
 QY 1861 AATGCTTTAGACAGTGTAAAAA 1884
 Db 46 AATGCTTTAGACAGTGTAAAA 23

RESULT 11
 US-09-999-997-11085/c
 : Sequence 11085, Application US/09699997
 : GENERAL INFORMATION:
 : APPLICANT: Curtiss, Rory A. J.
 : APPLICANT: Sllas-Santiago, Inmaculada
 : APPLICANT: Stefano, Peter
 : TITLE OF INVENTION: NOVEL NUCLEIC ACID MOLECULES AND USES
 : FILE REFERENCE: 1600.2020-001
 : CURRENT APPLICATION NUMBER: US/09/699, 997
 : PRIOR FILING DATE: 2000-10-30
 : PRIOR APPLICATION NUMBER: 60/162,359
 : NUMBER OF SEQ ID NOS: 12714
 : SOFTWARE: FASTSEQ for Windows Version 4.0
 : SEQ ID NO 11085
 : LENGTH: 1925
 : TYPE: DNA
 : ORGANISM: Homo sapiens
 US-09-999-997-11085

Query Match 98.2%; Score 1863.2; DB 27; Length 1925;
 Best Local Similarity 99.6%; Pred. No. 0;
 Matches 1876; Conservative 2; Mismatches 5; Indels 1; Gaps 1;
 QY 1 GCCAATCTCCGAGGCTGTGCTGCTGCGCCGCGAGAGCGGAGCGGAGAGAGAGAGAGCCG 60
 Db 1905 GCCAATCTCCGAGGCGC -GGTGTCTGCGCCGCGAGCGGAGCGGAGAGAGAGAGAGCCG 1847
 QY 61 CACCGGAGAGCGGAGGCGGAGGCGATGAGGCTCGGAGGAGGAGGAGGAGGAGGAGGAGG 120
 Db 1846 CACCGGAGAGCGGAGGCGGAGGCGATGAGGCTCGGAGGAGGAGGAGGAGGAGGAGG 1787
 QY 121 AGGTAGACGCTGTCTCCGCGAGAGAGCGGCGCCAGCAGGCTGGGAGGAGGAGGAGG 180
 Db 1786 AGGTAGACGCTGTCTCCGCGAGAGAGCGGCGCCAGCAGGCTGGGAGGAGGAGGAGG 1727
 QY 181 CGGTGAGCGGCGGAGGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 240
 Db 1726 CGGTGAGCGGCGGAGGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1667
 QY 241 GCCCGGAGAGCTCGGAGAGTGTGCTCTAGGATGCGGAGAGGAGGAGGAGGAGGAGGAG 300
 Db 1666 GCCCGGAGAGCTCGGAGAGTGTGCTCTAGGATGCGGAGAGGAGGAGGAGGAGGAGG 1607
 QY 301 CTGCTTCCAGGCTTGTGCTGCAAAATCAGTGTCTACAGTGTGAGAGATTTCCAGAGTGA 360
 Db 1606 CTGCTTCCAGGCTTGTGCTGCAAAATCAGTGTCTACAGTGTGAGAGATTTCCAGAGTGA 1547

QY 361 CAACGACTGCTCTCCCGGAGTTCAATGTGAATTCAGAGGAGGAGGAGGAGGAGGAGGAGG 420
 Db 1546 CAACGACTGCTCTCCCGGAGTTCAATGTGAATTCAGAGGAGGAGGAGGAGGAGGAGGAGG 1487
 QY 421 TCAGAAAGAGTGTAGAGCAAAAGTGGCGGATCATGTACGCAAGTCTGTGATCATC 480
 Db 1486 TCAGAAAGAGTGTAGAGCAAAAGTGGCGGATCATGTACGCAAGTCTGTGATCATC 1427
 QY 481 AGGCGCTGTCTATGCGCTTGTGCGGATACAGTCTTGTGCTTCCAGGAGAACTGAA 540
 Db 1426 AGGCGCTGTCTATGCGCTTGTGCGGATACAGTCTTGTGCTTCCAGGAGAACTGAA 1367
 QY 541 CTCAGTTGATGATGCTGTGCAACACCCCTTTGTAAGCGGAGGAGGAGGAGGAGGAGGAG 600
 Db 1366 CTCAGTTGATGATGCTGTGCAACACCCCTTTGTAAGCGGAGGAGGAGGAGGAGGAGGAG 1307
 QY 601 GGGAAAGTTCTGCTCGGCGCCCTCAGGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 660
 Db 1306 GGGAAAGTTCTGCTCGGCGCCCTCAGGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1247
 QY 661 AGCCCTTCTCGGAGACAGTGTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 720
 Db 1246 AGCCCTTCTCGGAGACAGTGTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1187
 QY 721 TTCCAGCCCTCGGCGCCACCCCTCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 780
 Db 1186 TTCCAGCCCTCGGCGCCACCCCTCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1127
 QY 781 AATCTGGGTAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 840
 Db 1126 AATCTGGGTAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1067
 QY 841 CTGCGTAAAGCATTTCTGAATTAATTCAGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTG 900
 Db 1066 CTGCGTAAAGCATTTCTGAATTAATTCAGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTG 1007
 QY 901 AGGAGGTGAGTGAATAATTCACCCCATGTCTGTGTAACCGAGTGTGAGGAGGAGGAGG 960
 Db 1006 AGGAGGTGAGTGAATAATTCACCCCATGTCTGTGTAACCGAGTGTGAGGAGGAGGAGG 947
 QY 961 AGAGTGTGCTTGAAGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTG 1020
 Db 946 AGAGTGTGCTTGAAGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTG 887
 QY 1021 CATTCATCCCTGATGGGAGGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGT 1080
 Db 886 CATTCATCCCTGATGGGAGGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGT 827
 QY 1081 GGCTGAGGAGGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTG 1140
 Db 826 GGCTGAGGAGGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTG 767
 QY 1141 GAAACCATTTCTGCAAGCAATTTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGT 1200
 Db 766 GAAACCATTTCTGCAAGCAATTTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGT 707
 QY 1201 CGAGACTCAATGATGAGGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGT 1260
 Db 706 CGAGACTCAATGATGAGGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGT 647
 QY 1261 AATCTTCTCAGTGTCTCTTGAAGAGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGT 1320
 Db 646 AATCTTCTCAGTGTCTCTTGAAGAGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGT 587
 QY 1321 GCACAAAGGAGGAGGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTG 1380
 Db 586 GCACAAAGGAGGAGGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTG 527
 QY 1381 TGCGTGTGTCAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1440
 Db 526 TGCGTGTGTCAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 467
 QY 1441 GCGAGGACACCGTGTACAGAGAGGAGGAGTGTGATGACCGAGTGTGAGTGTGAGTGTG 1500

|||||
Db 466 GCGAGACACCGCTGTACAGAGCGGGTGTATGACCGAGTGAAGTAAAGCTCTCCG 407
Qy 1501 AGAAGGGAGAGAGATCATGTACGCCCGAGTAGAGCTCGTCCAGTGTGGGTT 1560
Db 408 ACAAAGGGAGAGAGATCATGTACGCCCGAGTAGAGCTCGTCCAGTGTGGGTT 347
Qy 1561 TGGCCGACAGCTATGCTCTCCGATCTGTGGGATCCAGCATAGCGCAATGTACAA 1620
Db 346 TGGCCGACAGCTATGCTCTCCGATCTGTGGGATCCAGCATAGCGCAATGTACAA 287
Qy 1621 CATACGAGCTGTGGGAGACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1680
Db 286 CATACGAGCTGTGGGAGACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 227
Qy 1681 GAGAACACAGTAAATGAATTAATTAATTAATTAATTAATTAATTAATTAATTA 1740
Db 226 GAGAACACAGTAAATGAATTAATTAATTAATTAATTAATTAATTAATTAATTA 167
Qy 1741 GCGAGAAATGTATCCATTTTTCAGTGTGACCTGACAGCTTCTTTGGCCAGCA 1800
Db 166 GCGAGAAATGTATCCATTTTTCAGTGTGACCTGACAGCTTCTTTGGCCAGCA 107
Qy 1801 GAGAAATTTAAACACTGTTCACAAACCGGGAGTGGCTGTGTAAAGAAAGCAATTA 1860
Db 106 GAGAAATTTAAACACTGTTCACAAACCGGGAGTGGCTGTGTAAAGAAAGCAATTA 47
Qy 1861 AATGCTTAGACAGTGTAAAAAA 1884
Db 46 AATGCTTAGACAGTGTAAAA 23

RESULT 12

US-09-710-281-4458/c
; Sequence 4458, Application US/09710281
; GENERAL INFORMATION:
; APPLICANT: Hunter, John J.
; APPLICANT: Shyjan, Andrew W.
; APPLICANT: Stbdal, Hilde
; TITLE OF INVENTION: NOVEL NUCLEIC ACID MOLECULES AND USES
; FILE REFERENCE: 1600.2036-001
; CURRENT APPLICATION NUMBER: US/09/710,281
; CURRENT FILING DATE: 2000-11-10
; PRIOR APPLICATION NUMBER: 60/164,254
; PRIOR FILING DATE: 1999-11-09
; NUMBER OF SEQ ID NOS: 5803
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO: 4458
; LENGTH: 1925
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-710-281-4458

Query Match 98.2%; Score 1863.2; DB 28; Length 1925;
Best Local Similarity 99.6%; Pred. No. 0;
Matches 1876; Conservative 2; Mismatches 5; Indels 1; Gaps 1;

Qy 1 GCCAATCTCGGAGGCTGTGTGCTCGGCGGAGAGCGGAGGAGAGACAGACCCG 60
Db 1905 GCCAATCTCGGAGGCTGTGTGCTCGGCGGAGAGCGGAGGAGAGACAGACCCG 1847
Qy 61 CAGCCGGAGAGCGGAGGCGGAGATGACAGCTCCGAGAGCGGAGAGAGAGAGAGAG 120
Db 1846 CAGCCGGAGAGCGGAGGCGGAGATGACAGCTCCGAGAGCGGAGAGAGAGAGAG 1787
Qy 121 AGCTAGACAGCTGTCTCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 180
Db 1786 AGCTAGACAGCTGTCTCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1727
Qy 181 CGCTGACAGCGGAG 240
Db 1726 CGCTGACAGCGGAG 1667

Qy 241 GCCCGGAGACTCCGGAGAGATGTGGTCTTAGCATCGGCGCACTTTTGGGATGTT 300
Db 1666 GCCCGGAGACTCCGGAGAGATGTGGTCTTAGCATCGGCGCACTTTTGGGATGTT 1607
Qy 301 CTTCGCTTCAGAGCTTTCGCGCTGCAATTCAGTGTACAGTGTGAAGAAATTCAGCTGA 360
Db 1606 CTTCGCTTCAGAGCTTTCGCGCTGCAATTCAGTGTACAGTGTGAAGAAATTCAGCTGA 1547
Qy 361 CAAGACTGCTCTCTCCCGAGCTTCAATTTGAATTCAGAGGTAAAGCTTCAAGACTGTG 420
Db 1546 CAAGACTGCTCTCTCCCGAGCTTCAATTTGAATTCAGAGGTAAAGCTTCAAGACTGTG 1487
Qy 421 TCAGAAAGATGATGATGAGCAAGTCCGGAGATCATGTACCGCAATTCCTGTGATCATC 480
Db 1486 TCAGAAAGATGATGATGAGCAAGTCCGGAGATCATGTACCGCAATTCCTGTGATCATC 1427
Qy 481 AGCGGCTGTCTCATGCTCTGCGGGTACAGTCTCTCTCTCCCGAGAGAACTGA 540
Db 1426 AGCGGCTGTCTCATGCTCTGCGGGTACAGTCTCTCTCTCCCGAGAGAACTGA 1367
Qy 541 CTGAGTTTGCATGAGCTGCTGCAACACCCCTCTTTGTAACGGGCCAAGGCCAAGAAAG 600
Db 1366 CTGAGTTTGCATGAGCTGCTGCAACACCCCTCTTTGTAACGGGCCAAGGCCAAGAAAG 1307
Qy 601 GGGAGTTCGAGCTCGAGCCCTCAGGCGAGGCTCCGACACCATCTGTCTCAAAAT 660
Db 1306 GGGAGTTCGAGCTCGAGCCCTCAGGCGAGGCTCCGACACCATCTGTCTCAAAAT 1247
Qy 661 AGCCCTCTCTCGGCACTGTGAAAGCTGAAGAGTGAAGAGTGAAGAGTGAAGAGTGA 720
Db 1246 AGCCCTCTCTCGGCACTGTGAAAGCTGAAGAGTGAAGAGTGAAGAGTGAAGAGTGA 1187
Qy 721 TTCACGCTTCGCGCCCAACCCCAACCTCCGAGTGAATTCCTGTGGGTGCTTT 780
Db 1186 TTCACGCTTCGCGCCCAACCCCAACCTCCGAGTGAATTCCTGTGGGTGCTTT 1127
Qy 781 ATTCTGGGTAGGAGAGGAGAGTCCGTTCTCTTTGTTCTGTGCAATTAATGAAGAG 840
Db 1126 ATTCTGGGTAGGAGAGGAGAGTCCGTTCTCTTTGTTCTGTGCAATTAATGAAGAG 1067
Qy 841 CTCGGTAAGCAATTCGAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 900
Db 1066 CTCGGTAAGCAATTCGAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 1007
Qy 901 AGGAGGTGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGA 960
Db 1006 AGGAGGTGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGA 947
Qy 961 AGAGTGTGCTTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGA 1020
Db 946 AGAGTGTGCTTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGA 887
Qy 1021 CATTCATCTCTGATGAGGAGGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 1080
Db 886 CATTCATCTCTGATGAGGAGGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 827
Qy 1081 GGCCTGAGGAGGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 1140
Db 826 GGCCTGAGGAGGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 767
Qy 1141 GAAAGCAATTCCTGAGAGCAATTCCTGAGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGA 1200
Db 766 GAAAGCAATTCCTGAGAGCAATTCCTGAGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGA 707
Qy 1201 CGAGACTCAATGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGA 1260
Db 706 CGAGACTCAATGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 647
Qy 1261 AAATCTTCTGAGTTCCTCTTGAAGAGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 1320
Db 646 AAATCTTCTGAGTTCCTCTTGAAGAGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 587

Qy	1321	GCACAAGGGGGGCTGTGCGTGTGTGGAGTGGCCATGTACGGCAGGGCGCTTCGTGGT	1380
Db	586	GCACAAGGGGGGCGCTGTGCGTGTGTGGAGTGGCCATGTACGGCAGGGCGCTTCGTGGT	527
Qy	1381	TGGCGTGTCTGCAAGCGAGCGGGCGACACAGCACCTGTACAGAACACCCGGCGAAACTGCT	1440
Db	526	TGGCGTGTCTGCAAGCGAGCGGGCGACACAGCACCTGTACAGAACACCCGGCGAAACTGCT	467
Qy	1441	GGGAGGACACCGTGTACAGGAGCGGGTGTGATGACCGAGCTGAGGTAGAAAAACGTCCG	1500
Db	466	GGGAGGACACCGTGTACAGGAGCGGGTGTGATGACCGAGCTGAGGTAGAAAAACGTCCG	407
Qy	1501	AGAAAGGGGAGGAGATCATGTACGGCCCGGAAGTAGAGACCTCTGTCCACTGTGGGTT	1560
Db	406	AGAAAGGGGAGGAGATCATGTACGGCCCGGAAGTAGAGACCTCTGTCCACTGTGGGTT	347
Qy	1561	TGGCGGCACACCATGATCTCTCCGATCTGTGTGGGCATCCAGCATACGGCCCATGTCCAA	1620
Db	346	TGGCGGCACACCATGATCTCTCCGATCTGTGTGGGCATCCAGCATACGGCCCATGTCCAA	287
Qy	1621	CAATCACCCCTGGGCGAGACACGACGAGGAGGAGAGACAGAAAAAGAAAAACACAGCAT	1680
Db	286	CAATCACCCCTGGGCGAGACACGACGAGGAGGAGAGACAGAAAAAGAAAAACACAGCAT	227
Qy	1681	GAGAACACAGTAAATGAATAAAAACCATAAATATTTAGCCCTCTGTCTGTGCTTACTG	1740
Db	226	GAGAACACAGTAAATGAATAAAAACCATAAATATTTAGCCCTCTGTCTGTGCTTACTG	167
Qy	1741	GCCAGGAAATGTTACCAATTTTTCAGTGTGACCTGACAGCTCTCTTTGCCAACACCA	1800
Db	166	GCCAGGAAATGTTACCAATTTTTCAGTGTGACCTGACAGCTCTCTTTGCCAACACCA	107
Qy	1801	GAGAGAAATTTAACACTGTTTCAAACCCGGGGAGTGTGGCTGTTTAAAGAAAGACCTTA	1860
Db	106	GAGAGAAATTTAACACTGTTTCAAACCCGGGGAGTGTGGCTGTTTAAAGAAAGACCTTA	47
Qy	1861	AATGCTTTAGACAGTGTAAAAAA 1884	
Db	46	AATGCTTTAGACAGTGTATTTAA 23	

```

RESULT 13
US-09-726-805-1608/c
: Sequence 1608, Application US/09726805
: GENERAL INFORMATION:
: APPLICANT: Gearing, David P.
: APPLICANT: Holtzman, Douglas A.
: TITLE OF INVENTION: NOVEL NUCLEIC ACID MOLECULES AND USES
: TITLE OF INVENTION: THEREFOR
: FILE REFERENCE: 1600.2017-001
: CURRENT APPLICATION NUMBER: US/09/726,805
: CURRENT FILING DATE: 2000-11-30
: PRIOR APPLICATION NUMBER: 60/168,140
: PRIOR FILING DATE: 1999-11-30
: NUMBER OF SEQ ID NOS: 2158
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 1608
: LENGTH: 1925
: TYPE: DNA
: ORGANISM: Homo sapiens
US-09-726-805-1608

Query Match          98.2%      Score 1863.2;   DB 29;   Length 1925;
Best Local Similarity 99.6%      Pred. NO. 0;
Matches 1876; Conservative 2; Mismatches 5; Indels 1; Gaps 1.

QY      1  GCCAACTCCGAGAGCTCTGTGTCCTGGCCCGGAGACGCGAGCGGGAGAGAGCAGACGCCG 60
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Db      1305  GCCAACTCCGAGAGCGGC-GGTGCTCGGCCCGGAGACGCGAGCGGGAGAGAGACGCCG 1847

QY      61  CAGCGGGAGGCCGAGCGCGCGGCAGATGCAGAGCTCCGCGAGCGGACACTCGGCTCCTCTA 120
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Db      1846  CAGCGGGAGGCCGAGCGCGCGGCAGATGCAGAGCTCCGCGAGCGGACACTCGGCTCCTCTA 1787

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QY	121	AGCTACGACCGGTGCTGCTCCGCGGAGACGAGCGGGCGCCCAAGACGCTCGGACACAC	180
Db	1786	AGCTACGACCGGTGCTGCTCCGCGGAGACGAGCGGGCGCCCAAGACGCTCGGACACAC	1722
QY	181	CGCTGCACCGCGGGACACCTCCGCTGCTGCGGCTCCTCTGAGTGCCTTGGCCCTCCCG	240
Db	1726	CGCTGCACCGCGGGACACCTCCGCTGCTGCGGCTCCTCTGAGTGCCTTGGCCCTCCCG	166
QY	241	GCCCCGGGACTCCGGGAGAAATGTGCGTCTAGGCATCGCGGCAACTTTTTCGGATGT	300
Db	1666	GCCCCGGGACTCCGGGAGAAATGTGCGTCTAGGCATCGCGGCAACTTTTTCGGATGT	1607
QY	301	CTTGCTTCACAGGCTTTTCGCGGCAAAATCCAGTCTACAGTGTGAAGAAATTCACGTGA	360
Db	1606	CTTGCTTCACAGGCTTTTCGCGTGCATATCCAGTCTACAGTGTGAAGAAATTCACGTGA	154.47
QY	361	CAACGACTGCTCTCCCGGAGTTTCATTGTGAATTCACAGGTACAGTCAAGACATGTG	420
Db	1546	CAACGACTGCTCTCCCGGAGTTTCATTGTGAATTCACAGGTACAGTCAAGACATGTG	1487
QY	421	TCAGAAAGAAATGTATGGAGAAATGCCGGGATCATATGTACGCCAATCTCTGTGCATATC	480
Db	1486	TCAGAAAGAAATGTATGGAGAAATGCCGGGATCATATGTACGCCAATCTCTGTGCATATC	1422
QY	481	AGCGCGCTGCTCATCTCCCTTCGCGGGATACAGTCTTCTGCTCCCAAGGAAATCTGA	540
Db	1426	AGCGCGCTGCTCATCTCCCTTCGCGGGATACAGTCTTCTGCTCCCAAGGAAATCTGA	1367
QY	541	CTCAGTTTGCATCAGCTGCTGCAACACCCCTCTTGTAAACGGGCCAAGGCCCAAGAAAG	600
Db	1366	CTCAGTTTGCATCAGCTGCTGCAACACCCCTCTTGTAAACGGGCCAAGGCCCAAGAAAG	1307
QY	601	GGGAAAGTTGCGCCCTCGGCCCTCGAGGCGAGGCGCGCACACCATCTGTCTCTCAAAAT	660
Db	1306	GGGAAAGTTGCGCCCTCGGCCCTCTCAGGCGAGGCGCTCCGACACCATCTGTCTCTCAAAAT	124.47
QY	661	AGCCCTCTTCTCGGACACTGCTGTAAGCTGAAAGAGATGCCACCCCTCTGCTCATTTGTC	720
Db	1246	AGCCCTCTTCTCGGACACTGCTGTAAGCTGAAAGAGATGCCACCCCTCTGCTCATTTGTC	1187
QY	721	TTTCAGGCGCTCGGCCCAACCCCCCAACCTCCCTGATGATGTTCTTCTGCGTCCCTT	780
Db	1186	TTTCAGGCGCTCGGCCCAACCCCCCAACCTCCCTGATGATGTTCTTCTGCGTCCCTT	1122
QY	781	ATTCTGGGTAGGAGCGGAGTCCGATGCTCTTTTGTCTCTGTGCAAAATATGAAGAG	840
Db	1126	ATTCTGGGTAGGAGCGGAGTCCGATGCTCTTTTGTCTCTGTGCAAAATATGAAGAG	1067
QY	841	CTCGGTAAAGCATTTCTGTAATTAATTCAGCTGACGTGAATTTTCAGTATGTACTGAAGA	900
Db	1066	CTCGGTAAAGCATTTCTGTAATTAATTCAGCTGACGTGAATTTTCAGTATGTACTGAAGA	1007
QY	901	AGGAGGTGAGAGTAAAGTTTACCCCATGCTGTGTAAACGGAGTCAAGGCCAGGCTGCG	960
Db	1006	AGGAGGTGAGAGTAAAGTTTACCCCATGCTGTGTGTAAACGGAGTCAAGGCCAGGCTGCG	947
QY	961	AGAGTCTGCTTGAAGTCACTGAGGTGGGACATCTGCTTTTGTAAAGCCCTCCAGTGT	1020
Db	946	AGAGTCTGCTTGAAGTCACTGAGGTGGGACATCTGCTTTTGTAAAGCCCTCCAGTGT	887
QY	1021	CATTCCATCCCTATATGGGGCATATGTTTGAAGCTGAGAGTGAAGTGAACGTTTCTTAG	1080
Db	886	CATTCCATCCCTATATGGGGCATATGTTTGAAGCTGAGAGTGAAGTGAACGTTTCTTAG	827
QY	1081	GCGTGAAGGGCCAGTTCCACTCAAGCTCCCTCGCTTGACATTCATAACTTCATCTCT	1140
Db	826	GCGTGAAGGGCCAGTTTCCACTCAAGCTCCCTCGCTTGACATTCATAACTTCATCTCT	767
QY	1141	GAAGAACATTTCTGAGACAGAAATGTGCTGTTTGGCGCTGAGTGTGGGCTCTAGTACT	1200
Db	766	GAAGAACATTTCTGAGACAGAAATGTGCTGTTTGGCGCTGAGTGTGGGCTCTAGTACT	707

OY	960	CAGAGTCOMGTCCTTAAAGACACCTGAGGTTGGGCACTGTGCTTTTGTAAAGCTCCAGAGT	1015
Db	975	CAGAGTCAGTCCTTAAAGACACCTGAGGTTGGGCACTGTGCTTTTGTAAAGCTCCAGAGT	1034
OY	1020	CCATTCATCCCTGATGATGGGGGCACTACTTTTGAGACTGCAAGAGTGAGACGTGACTTTCTTA	1079
Db	1035	CCATTCATCCCTGATGATGGGGGCACTACTTTTGAGACTGCAAGAGTGAGACGTGACTTTCTTA	1094
OY	1080	GGGCTGAGGGGCCAGTTCCCACTCAAGGCTCCCTGGCTTGACATTTCAAACTTCATGCTCC	1139
Db	1095	GGGCTGAGGGGCCAGTTCCCACTCAAGGCTCCCTGGCTTGACATTTCAAACTTCATGCTCC	1154
OY	1140	TGAAACCACTTCCTGTGAGCAGAAATTGGCTGGTTGGCCCTGAGATGGGCTCAAGTGAC	1199
Db	1155	TGAAACCACTTCCTGTGAGCAGAAATTGGCTGGTTGGCCCTGAGATGGGCTCAAGTGAC	1214
OY	1200	TGCGAGACTCAATGACTGGAGCTTAGACTGAGGCTGGGCTCGGCTCTGAAAAGTGCTTAAG	1259
Db	1215	TGCGAGACTCAATGACTGGAGCTTAGACTGAGGCTGGGCTCGGCTCTGAAAAGTGCTTAAG	1274
OY	1260	AAAAATCTTCTCAGTTCTCTCTTGACAGAGACCTGGCGCGGGAGCGGAGAAGCAAGCGGCGC	1319
Db	1275	AAAAATCTTCTCAGTTCTCTCTTGACAGAGACCTGGCGCGGGAGCGGAGAAGCAAGCGGCGC	1334
OY	1320	TGCAACAAAGGGGGGGCGTGGTGGGTGGAGTGGCATGTAGCGGAGGGGCGTCTCTGCGGG	1379
Db	1335	TGCAACAAAGGGGGGGCGTGGTGGGTGGAGTGGCATGTAGCGGAGGGGCGTCTCTGCGGG	1394
OY	1380	TTGGCGTGCTGCACAGCGACGAGCGGCGAGCAAGCAGCTCGACACACACCOCGCGAAATGTC	1439
Db	1395	TTGGCGTGCTGCACAGCGACGAGCGGCGAGCAAGCAGCTCGACACACACCOCGCGAAATGTC	1454
OY	1440	TGCGAGGACACCGTGTACAGAGACGGGGTTGATGACCGAGCTAGAGTAAAAAGCTCTCC	1499
Db	1455	TGCGAGGACACCGTGTACAGAGACGGGGTTGATGACCGAGCTAGAGTAAAAAGCTCTCTCC	1514
OY	1500	GAGAAAGGGGAGAGATCATGTACGGCCGGGAATAGAGACTGTGTCOAGTCGTCGTGGGT	1559
Db	1515	GAGAAAGGGGAGAGATCATGTACGGCCGGGAATAGAGACTGTGTCOAGTCGTCGTGGGT	1574
OY	1560	TTGGCCGAGCAGATGATCTCCGAATCTGGTTGGGANTCAGACATACGGCCATGTGCACA	1619
Db	1575	TTGGCCGAGCAGATGATCTCCGAATCTGGTTGGGANTCAGACATACGGCCATGTGCACA	1634
OY	1620	ACAATCAGCCTTGCGGACACGACGACGAGGAGAGACAGAGAAAGAAAAACACAGCA	1679
Db	1635	ACAATCAGCCTTGCGGACACGACGACGAGGAGAGACAGAGAAAGAAAAACACAGCA	1694
OY	1680	TGAGAACACAGTAATGAATAAATAAACCATTAATAATTTAGCCCTCGTCTGTGCTGCTACT	1739
Db	1695	TGAGAACACAGTAATGAATAAATAAACCATTAATAATTTAGCCCTCGTCTGTGCTGCTACT	1754
OY	1740	GGCCAGGAAATGATACCAATTTTCTAGTGTGGACTTTGACAGCTTCTTTGGCACAAAGCA	1799
Db	1755	GGCCAGGAAATGATACCAATTTTCTAGTGTGGACTTTGACAGCTTCTTTGGCACAAAGCA	1814
OY	1800	AGAGAGAAATTTAACACCTGTTTCAAAACCCGGGGAGTTGGCTGTGTTAAAGAAAGCCATT	1859
Db	1815	AGAGAGAAATTTAACACCTGTTTCAAAACCCGGGGAGTTGGCTGTGTTAAAGAAAGCCATT	1874
OY	1860	AAATGCTTTAGACAGTGTA 1878	
Db	1875	AAATGCTTTAGACAGTGTA 1893	

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Job time : 4256.79 secs

GenCore version 5.1.3
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OM nucleic - nucleic search, using sw model

Run on: November 7, 2002, 10:10:48 ; Search time 52.9982 Seconds
(without alignments)
3937.596 Million cell updates/sec

Title: US-09-970-966-214

Perfect score: 1897

Sequence: 1 gccacccgcgagctctg.....aaaaaaaaaaaaaaaaaa 1897

Scoring table: IDENTITY_NUC
Gapop 10.0, Gapext 1.0

Searched: 193892 seqs, 55004114 residues

Total number of hits satisfying chosen parameters: 387784

Minimum DB seq length: 0
Maximum DB seq length: 200000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1523.2	80.3	1524	6	US-10-230-437-15
2	46	2.4	2196	6	US-10-270-333-38
3	46	2.4	6472	6	US-10-270-333-37
4	45	2.4	667	7	US-60-416-172-67
5	44.6	2.4	4563	6	US-10-125-923A-311
6	42	2.2	4526	6	US-10-240-965-86
7	41.8	2.2	1734	6	US-10-230-437-155
8	41.8	2.2	1734	6	US-10-125-923A-201
9	40.8	2.2	1289	6	US-10-274-177-9
10	40.2	2.1	836	6	US-10-240-965-254
11	40.2	2.1	3901	6	US-10-240-965-1425
12	39.8	2.1	1524	6	US-10-230-437-15
13	39.2	2.1	5715	6	US-10-240-965-357
14	39	2.1	1901	6	US-10-145-087A-18
15	39	2.1	1901	6	US-10-143-031A-18
16	39	2.1	1901	6	US-10-145-092A-18
17	39	2.1	1901	6	US-10-162-522A-18
18	39	2.1	1901	6	US-10-165-038A-18
19	39	2.1	1901	6	US-10-165-353-18
20	39	2.1	1901	6	US-10-170-481A-18
21	39	2.1	1901	6	US-10-172-039A-18
22	39	2.1	1901	6	US-10-145-016A-18
23	39	2.1	1901	6	US-10-145-088A-18
24	39	2.1	1901	6	US-10-145-129A-18
25	39	2.1	1901	6	US-10-125-923A-47
26	39	2.1	1901	6	US-10-165-353A-18

27	38.6	2.0	1032	1	PCT-US02-12342-2	Sequence 2, Appl1
28	38.6	2.0	1149	1	PCT-US02-12342-1	Sequence 1, Appl1
29	38.6	2.0	1376	1	PCT-US02-12342-4	Sequence 4, Appl1
30	38.6	2.0	8906	6	US-10-240-851-85	Sequence 85, Appl1
31	38.4	2.0	610	6	US-10-264-237-199	Sequence 199, Appl
32	38.4	2.0	4098	6	US-10-240-425-1428	Sequence 1428, Ap
33	38.2	2.0	9889	6	US-10-270-333-196	Sequence 98, Appl
34	38	2.0	1251	6	US-10-270-333-98	Sequence 97, Appl
35	38	2.0	9268	6	US-10-270-333-97	Sequence 82, Appl
36	37.6	2.0	2954	6	US-10-240-965-82	Sequence 161, App
37	37.4	2.0	4034	6	US-10-240-965-161	Sequence 115, App
38	37.4	2.0	5927	6	US-10-270-333-115	Sequence 73, Appl
39	36.6	1.9	3305	6	US-10-145-087A-73	Sequence 73, Appl
40	36.6	1.9	3305	6	US-10-143-031A-73	Sequence 73, Appl
41	36.6	1.9	3305	6	US-10-145-092A-73	Sequence 73, Appl
42	36.6	1.9	3305	6	US-10-162-522A-73	Sequence 73, Appl
43	36.6	1.9	3305	6	US-10-165-038A-73	Sequence 73, Appl
44	36.6	1.9	3305	6	US-10-165-353-73	Sequence 73, Appl
45	36.6	1.9	3305	6	US-10-170-481A-73	Sequence 73, Appl

ALIGNMENTS

RESULT 1
US-10-230-437-15
Sequence 15, Application US/10230437
GENERAL INFORMATION:
APPLICANT: Baker, Kevin P.
APPLICANT: Desnoyers, Luc
APPLICANT: Geriltsen, Mary
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Smith, Victoria
APPLICANT: Stephan, Jean-Philippe F.
APPLICANT: Watanabe, Colin L.
APPLICANT: Wood, William I.
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
FILE REFERENCE: P3530PIC94
CURRENT APPLICATION NUMBER: US/10/230,437
CURRENT FILING DATE: 2002-08-28
PRIOR APPLICATION NUMBER: 10/119,480
PRIOR FILING DATE: 2002-04-09
PRIOR APPLICATION NUMBER: 60/059113
PRIOR FILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/062287
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/063549
PRIOR FILING DATE: 1997-10-28
PRIOR APPLICATION NUMBER: 60/064103
PRIOR FILING DATE: 1997-10-31
PRIOR APPLICATION NUMBER: 60/069873
PRIOR FILING DATE: 1997-12-17
PRIOR APPLICATION NUMBER: 60/078910
PRIOR FILING DATE: 1998-03-20
PRIOR APPLICATION NUMBER: 60/079294
PRIOR FILING DATE: 1998-03-25
PRIOR APPLICATION NUMBER: 60/079656
PRIOR FILING DATE: 1998-03-26
PRIOR APPLICATION NUMBER: 60/079788
PRIOR FILING DATE: 1998-03-27
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 246
SEQ ID NO 15
LENGTH: 1524
TYPE: DNA
ORGANISM: Homo Sapien
US-10-230-437-15
Query Match 80.3%; Score 1523.2; DB 6; Length 1524;


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Db      38 CTTGGGCGCTGGGCTTAATTGAGGTCCCGAGGGTCCAAAGCTCTGGGTTGAGAGGGGG 97
Qy      75 AGCGGGGCGATGAGAGTCCGCGAGCGGCACTCGGCTCTCTAAGCTACGACCGTCG 134
Db      98 GGGCGGAGGGGGGCTGTCTTCCAAAGGGCGGGTCCCGGGGTCTCTGAAGGCGGAGCA 157
Qy      135 TCTCCGGGAGCAGAGCGGGGGCCAGAGCTTCGAGCAGCCGCTGACCGCGGG 194
Db      158 GGGCGGATTCACCACTGTCTGCGCTGAGCGCGTGGCGGGCCAGCGGCTGCGCTGCA 217
Qy      195 CAGGCTCGGCTGTCTG 211
Db      218 CCGGACCGGAGCGCGC 234

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RESULT 11 US-10-240-425-1425/c

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; GENERAL INFORMATION:
; APPLICATION: US/10240425
; APPLICANT: Williams, Amanda
; APPLICANT: Boland, Joseph F.
; APPLICANT: Lord, Reginald V.
; APPLICANT: Alvarez, Chris
; APPLICANT: Metzel, Jon C.
; APPLICANT: Scherf, Uwe
; APPLICANT: Vockley, Joseph G.
; TITLE OF INVENTION: Gene Expression Profiles in Esophageal Tissue
; FILE REFERENCE: 44921-5026
; CURRENT APPLICATION NUMBER: US/10/240,425
; CURRENT FILING DATE: 2002-09-30
; PRIOR APPLICATION NUMBER: PCT/US01/09847
; PRIOR FILING DATE: 2001-03-28
; PRIOR APPLICATION NUMBER: US 60/193,446
; PRIOR FILING DATE: 2000-03-31
; NUMBER OF SEQ ID NOS: 1588
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1425
; LENGTH: 3901
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: Genbank Accession No. U25997
US-10-240-425-1425

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Query Match
Best Local Similarity 57.6%; Score 40.2; DB 6; Length 3901;
Matches 72; Conservative 0; Mismatches 53; Indels 0; Gaps 0;

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Qy      138 CCGGCGAGCAGGCGGGGCCCGCCAGCAGCCGCGAGCCGCGAGCCGCGGAG 197
Db      125 CTGCTGCTGCGACCGGTGCTCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 66
Qy      198 CTTCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 257
Db      65 CCACCGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 6
Qy      258 GAATG 262
Db      5 AACTG 1

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RESULT 12 US-10-230-437-15/c

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; GENERAL INFORMATION:
; APPLICATION: US/10230437
; APPLICANT: Baker, Kevin P.
; APPLICANT: Desnoyers, Luc
; APPLICANT: Gerritsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.

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; APPLICANT: Smith, Victoria
; APPLICANT: Stephan, Jean-Philippe F.
; APPLICANT: Watanabe, Colin L.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3530P1C94
; CURRENT APPLICATION NUMBER: US/10/230,437
; CURRENT FILING DATE: 2002-08-28
; PRIOR APPLICATION NUMBER: 10/119,480
; PRIOR FILING DATE: 2002-04-09
; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/062287
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/063549
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/064103
; PRIOR FILING DATE: 1997-10-31
; PRIOR APPLICATION NUMBER: 60/069873
; PRIOR FILING DATE: 1997-12-17
; PRIOR APPLICATION NUMBER: 60/078910
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/079294
; PRIOR FILING DATE: 1998-03-25
; PRIOR APPLICATION NUMBER: 60/079656
; PRIOR FILING DATE: 1998-03-26
; PRIOR APPLICATION NUMBER: 60/079728
; PRIOR FILING DATE: 1998-03-27
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 246
; SEQ ID NO 15
; LENGTH: 1524
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-230-437-15

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Query Match
Best Local Similarity 67.5%; Score 39.8; DB 6; Length 1524;
Matches 56; Conservative 0; Mismatches 27; Indels 0; Gaps 0;

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Qy      143 GCAGCAGCGCGGGCCCGCAGAGCTTCGCGAGCCGCGTGCAGCGCGGAGCGCTCC 202
Db      86 GCATCAGAGGAGCGAGCAGCAGCGAGCGAGCGTCCCGGCTGCGAGGCGTGTGCTCCGAG 27
Qy      203 GCTGCTGCTGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 225
Db      26 GCTGCTGCGGCGCGCGCTGCTG 4

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; GENERAL INFORMATION:
; APPLICATION: US/10240425
; APPLICANT: Williams, Amanda
; APPLICANT: Boland, Joseph F.
; APPLICANT: Lord, Reginald V.
; APPLICANT: Alvarez, Chris
; APPLICANT: Metzel, Jon C.
; APPLICANT: Scherf, Uwe
; APPLICANT: Vockley, Joseph G.
; TITLE OF INVENTION: Gene Expression Profiles in Esophageal Tissue
; FILE REFERENCE: 44921-5026
; CURRENT APPLICATION NUMBER: US/10/240,425
; CURRENT FILING DATE: 2002-09-30
; PRIOR APPLICATION NUMBER: PCT/US01/09847
; PRIOR FILING DATE: 2001-03-28
; PRIOR APPLICATION NUMBER: US 60/193,446
; PRIOR FILING DATE: 2000-03-31
; NUMBER OF SEQ ID NOS: 1588
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 357
; LENGTH: 5715

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TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: Genbank Accession No. AB023157
US-10-240-425-357

Query Match
Best Local Similarity 54.1%; Score 39.2; DB 6; Length 5715;
Pred. No. 1.6;
Matches 80; Conservative 0; Mismatches 68; Indels 0; Gaps 0;

QY 100 GCGGCACTGCGGCTCTTAAGCTACGACCGCTCTCCGCGGACAGCGGCGCC 159
DB 532 GAGGCACTTCTCTCCGCAAGTGGCTGGCGGACGACGACGACGCGCGCGC 591
QY 160 AGAGCTGCGGACGACGACGCGGCGGCGGCGGCGGCGGCGGCGGCGGCG 219
DB 592 CGGCTGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 651
QY 220 TGATGCGCTTGCCTCTCCGCGGCGGCGGCGGCGGCGGCGGCGGCGG 247
DB 652 AGCAGCGCGCTCACCAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 679

RESULT 14
US-10-145-087A-18
Sequence 18, Application US/10145087A
GENERAL INFORMATION:

APPLICANT: Ashkenazi, Avi
APPLICANT: Baker Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan
APPLICANT: Ferrara, Napoleon
APPLICANT: Filvaroff, Ellen
APPLICANT: Fong, Sherman
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerltsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Hillan, Kenneth J.
APPLICANT: Kijavlin, Ivar J.
APPLICANT: Kuo, Sophia S.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Shelton, David L.
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2630P1C47
CURRENT APPLICATION NUMBER: US/10/145,087A
CURRENT FILING DATE: 2001-10-18
PRIOR APPLICATION NUMBER: 09/918585
PRIOR FILING DATE: 2001-07-30
PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/064249
PRIOR FILING DATE: 1997-11-03
PRIOR APPLICATION NUMBER: 60/065311
PRIOR FILING DATE: 1997-11-13
PRIOR APPLICATION NUMBER: 60/066364
PRIOR FILING DATE: 1997-11-21
PRIOR APPLICATION NUMBER: 60/077450
PRIOR FILING DATE: 1998-03-10
PRIOR APPLICATION NUMBER: 60/077632
PRIOR FILING DATE: 1998-03-11

PRIOR APPLICATION NUMBER: 60/077641
PRIOR FILING DATE: 1998-03-11
PRIOR APPLICATION NUMBER: 60/077649
PRIOR FILING DATE: 1998-03-11
PRIOR APPLICATION NUMBER: 60/077791
PRIOR FILING DATE: 1998-03-12
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 624
SEQ ID NO 18
LENGTH: 1901
TYPE: DNA
ORGANISM: Homo sapiens
US-10-145-087A-18

Query Match
Best Local Similarity 56.4%; Score 39; DB 6; Length 1901;
Pred. No. 1;
Matches 92; Conservative 0; Mismatches 70; Indels 1; Gaps 1;

QY 57 CCGGACCGGAGAGCCGAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCG 116
DB 9 CCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 68
QY 117 TCTAAGCTACGACCGCTCTCCGCGGACGACGCGGCGGCGGCGGCGGCGG 176
DB 69 TCCCTGCTGAGCTGCGGCTGCTGCGGCTGCGGCTGCGGCTGCGGCTGCGG 127
QY 177 CAGCGCTGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 219
DB 128 CTGCCCCCGCCAGCGGCACTTCCACCGTGAAGCCGCTCATCTTC 170

RESULT 15
US-10-143-031A-18
Sequence 18, Application US/10143031A
GENERAL INFORMATION:

APPLICANT: Ashkenazi, Avi
APPLICANT: Baker Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan
APPLICANT: Ferrara, Napoleon
APPLICANT: Filvaroff, Ellen
APPLICANT: Fong, Sherman
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerltsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Hillan, Kenneth J.
APPLICANT: Kijavlin, Ivar J.
APPLICANT: Kuo, Sophia S.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Shelton, David L.
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2630P1C39
CURRENT APPLICATION NUMBER: US/10/143,031A
CURRENT FILING DATE: 2002-10-10
PRIOR APPLICATION NUMBER: 09/918585
PRIOR FILING DATE: 2001-07-30
PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/064249
PRIOR FILING DATE: 1997-11-03

665

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; PRIOR APPLICATION NUMBER: 60/065311
; PRIOR FILING DATE: 1997-11-13
; PRIOR APPLICATION NUMBER: 60/066364
; PRIOR FILING DATE: 1997-11-21
; PRIOR APPLICATION NUMBER: 60/077450
; PRIOR FILING DATE: 1998-03-10
; PRIOR APPLICATION NUMBER: 60/077632
; PRIOR FILING DATE: 1998-03-11
; PRIOR APPLICATION NUMBER: 60/077641
; PRIOR FILING DATE: 1998-03-11
; PRIOR APPLICATION NUMBER: 60/077649
; PRIOR FILING DATE: 1998-03-11
; PRIOR APPLICATION NUMBER: 60/077791
; PRIOR FILING DATE: 1998-03-12
; Remaining Prior Application data removed - See file Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 624
; SEQ ID NO 18
; LENGTH: 1901
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-10-143-031A-18

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Query Match      2.1%; Score 39; DB 6; Length 1901;
Best Local Similarity 56.4%; Pred. No. 1;
Matches 92; Conservative 0; Mismatches 70; Indels 1; Gaps 1;

OY 57 CCCGACGCGGAGCCGCGAGCGGCGATGACAGCTCCGCGAGCGGACCTGGGCTCC 116
    ||| ||||| ||||| ||| | | | | | | | | | | | | | | | | | | |
Db 9  CCGGCGCGCGGCGCGCGAGCCGCGAGCCGCGATGCGGCGCTGCTGGAGCCTGC 68
    ||| ||||| ||||| ||| | | | | | | | | | | | | | | | | | | |

OY 117 TCTAAGCTACGACCGCTGCTCCGCGGCGAGCGGCGGCCCGACAGCCTGGGAGCCA 176
    ||| ||||| ||||| ||| | | | | | | | | | | | | | | | | | | |
Db 69 TCCCTGCTCAGCTGCGCGTC-CTGCTCTGCGGCTGCGCCCGTCGCAATGCTGTGACAGCTG 127
    ||| ||||| ||||| ||| | | | | | | | | | | | | | | | | | | |

OY 177 CAGCGCTGAGCGGCGGCGAGCCTCCGCTGCTGCGCTCTC 219
    ||| ||||| ||||| ||| | | | | | | | | | | | | | | | | | | |
Db 128 CTGCGCGCGAGCGGCGAGCTCAGCCGTGAGCGCGCTCATCTTC 170
    ||| ||||| ||||| ||| | | | | | | | | | | | | | | | | | | |

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Search completed: November 7, 2002, 18:02:24
 Job time : 85.9982 secs

GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: November 7, 2002, 09:52:52 ; Search time 2541.39 Seconds
(without alignments)
12088.985 Million cell updates/sec

Title: US-09-970-966-214

Perfect score: 1897
Sequence: 1 gccacactccgagagctctg.....aaaaaaaaaaaaaaaaaaaaa 1897

Scoring table: IDENTITY_MNC
Gapop 10.0 , Gapext 1.0

Searched: 16154066 seqs, 8097743376 residues

Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

EST:*
1: em_estba:*
2: em_estbm:*
3: em_estln:*
4: em_estlm:*
5: em_estov:*
6: em_estpl:*
7: em_estro:*
8: em_estr:*
9: gb_estl:*
10: gb_est2:*
11: gb_hic:*
12: gb_est3:*
13: gb_est4:*
14: gb_est5:*
15: em_estfun:*
16: em_estcom:*
17: gb_gss:*
18: em_gss_hum:*
19: em_gss_inv:*
20: em_gss_pln:*
21: em_gss_vrt:*
22: em_gss_fun:*
23: em_gss_mam:*
24: em_gss_mus:*
25: em_gss_other:*
26: em_gss_pro:*
27: em_gss_rod:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	798	42.1	888	14	B0689771
2	764.8	40.3	814	9	AL567376
3	741.2	39.1	920	9	AL538562
4	709.2	37.4	987	14	B0668420
5	700.8	36.9	821	12	BG752229
6	698.8	36.8	702	14	BQ006545

7	678.8	35.8	1490	11	AK012406
8	672.4	35.4	678	9	AI936826
9	672.4	35.4	696	13	BM547680
10	664.2	35.0	747	13	BI917149
11	658.8	34.7	799	10	BE271770
12	657.6	34.7	676	10	BE385990
13	651.4	34.3	704	13	BI919074
14	651.2	34.3	650	10	AM149665
15	645	34.0	658	13	BI554034
16	635	33.5	707	13	BI913989
17	630.4	33.2	690	13	BI669845
18	626.8	33.0	649	10	AM590950
19	624.4	32.9	627	13	BM669397
20	611.2	32.2	616	9	AI990500
21	610.4	32.2	696	12	BF439382
22	609.2	32.1	850	12	BE736301
23	608.4	32.1	645	12	BF432379
24	605.8	31.9	704	13	BI823714
25	602	31.7	743	10	BE395797
26	599.4	31.6	879	14	BO689033
27	591.2	31.2	654	12	BE746601
28	589	31.0	843	12	BF125134
29	587.4	31.0	531	9	AI884686
30	577.4	30.4	759	12	BF126050
31	569	30.0	948	14	BO882838
32	566.4	29.9	1010	12	BF345141
33	560.4	29.5	578	9	AI742092
34	558.8	29.5	699	10	BE395581
35	555.4	29.3	571	14	BM709964
36	550.8	29.0	670	12	BG753617
37	549.4	29.0	551	12	BE858216
38	538.4	28.4	540	12	BF396693
39	537	28.3	537	12	BF594242
40	533.8	28.1	538	13	BM667957
41	532.2	28.1	537	9	AI018769
42	530.8	28.0	534	10	BE350014
43	526.8	27.8	561	10	AM150789
44	526.8	27.8	589	9	AI859538
45	525.4	27.7	527	10	AM338938

ALIGNMENTS

RESULT 1
LOCUS B0689771 888 bp mRNA linear EST 15-JUL-2002
DEFINITION AGENCOCURT_8344092 NIH_MGC_110 Homo sapiens CDNA clone IMAGE:6248684
ACCESSION B0689771
VERSION B0689771
KEYWORDS 5', mRNA sequence.
SOURCE B0689771.1 GI:21815087
ORGANISM EST.
human.
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 888)
NIH-MGC http://mgi.ncl.nih.gov/
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgaabs-r@mail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at:
http://image.llnl.gov
Plate: L1CM2388 row: 0 column: 21
High quality sequence stop: 653.
Location/Qualifiers
1..888

FEATURES
Source

/organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone_image="6248684"
 /clone_1db="NIH_MGC_110"
 /tissue_type="ductal carcinoma, cell line"
 /lab_host="DH10B (phage-resistant)"
 /note="Organ: pancreas; Vector: pCMV7; Site: 1: XhoI;
 Site: 2: EcoRI; cDNA made by oligo-dT priming,
 directionally cloned into EcoRI/XhoI sites using the
 following 5' adaptor: GGCACAG(G). Library constructed by
 Ling Hong in the laboratory of Gerald M. Rubin (University
 of California, Berkeley) using ZAP-cDNA synthesis kit
 (Stratagene) and Superscript II RT (Life Technologies).
 Note: this is a NIH_MGC library."

BASE COUNT 217 a 219 c 264 g 187 t 1 others

ORIGIN

Query Match 42.1%; Score 798; DB 14; Length 888;
 Best Local Similarity 96.5%; Pred. No. 6.7e-134;
 Matches 856; Conservative 2; Mismatches 23; Indels 6; Gaps 4;

OY 850 GCATTCTGAATTAATTCAGCTGACTGAATTTTCACTATGACTTGAAGAAAGAGAGTGG 909
 DB 1 GCATTCTGAATTAATTCAGCTGACTGAATTTTCACTATGACTTGAAGAAAGAGAGTGG 60
 OY 910 AGTGAAGTTCACCCCATGCTGTGTACAGGAGTCAAGGCGAGCTGGCAGAGTCMGT 969
 DB 61 AGTGAAGTTCACCCCATGCTGTGTACAGGAGTCAAGGCGAGCTGGCAGAGTCMGT 120
 OY 970 CCTTAGAAGTCACTAGAGTGGGATCTGCTTTTGTAAAGCCTCCAGTGTCCATTCATC 1029
 DB 121 CCTTAGAAGTCACTAGAGTGGGATCTGCTTTTGTAAAGCCTCCAGTGTCCATTCATC 180
 OY 1030 CCTGATGGGGGATAGTTTGAACATGCAAGTACAGTCTTCTTGAAGGCTGGAG 1089
 DB 181 CCTGATGGGGGATAGTTTGAACATGCAAGTACAGTCTTCTTGAAGGCTGGAG 240
 OY 1090 GCCAGTTCACACTCAAGGCTCCCTGCTTGAATTAATTCATGCTCCCTGAAGAACAT 1149
 DB 241 GCCAGTTCACACTCAAGGCTCCCTGCTTGAATTAATTCATGCTCCCTGAAGAACAT 300
 OY 1150 TCTTCGACAGCAATGCTGCTTGGGCTGAGTGGGCTTCTAGTACTGACACTCA 1209
 DB 301 TCTTCGACAGCAATGCTGCTTGGGCTGAGTGGGCTTCTAGTACTGACACTCA 360
 OY 1210 ATGACGAGTCTAGACGCTGGGCTGCTGCTTGAAGGCTTGAAGAAATCTTCT 1269
 DB 361 ATGACGAGTCTAGACGCTGGGCTGCTGCTTGAAGGCTTGAAGAAATCTTCT 420
 OY 1270 CAGTTCCTTCAGAGGACTGGCGCGGAGCGCAAGACAGGCGGCTGCACAAAGC 1329
 DB 421 CAGTTCCTTCAGAGGACTGGCGCGGAGCGCAAGACAGGCGGCTGCACAAAGC 480
 OY 1330 GGGCGCTGTCGCTGCTGAGTGTGCGCATGACGCGGCGCTTCTGCTGTTGGCTGCT 1389
 DB 481 GGGCGCTGTCGCTGCTGAGTGTGCGCATGACGCGGCGCTTCTGCTGTTGGCTGCT 540
 OY 1390 GAGAGCAGAGGGGGGAGCAGACACTGACAGCAACCCGCGCAAACTGCTGGAGAGCA 1449
 DB 541 GAGAGCAGAGGGGGGAGCAGACACTGACAGCAACCCGCGCAAACTGCTGGAGAGCA 600
 OY 1450 CCGTGTACAGAGCGGCTGATGACCGAGCTGAGTGAAGAAACGCTCCGAGAAAGGGA 1509
 DB 601 CCGTGTACAGAGCGGCTGATGACCGAGCTGAGTGAAGAAACGCTCCGAGAAAGGGA 660
 OY 1510 GAGAGTATGTAAGCGCGGAAAGTAGAGCTGCTCCAGTGTGCTGCTGGCTGCTG 1568
 DB 661 GAGAGTATGTAAGCGCGGAAAGTAGAGCTGCTCCAGTGTGCTGCTGGCTGCTG 720
 OY 1569 GGCATATATCTCGAATCTGCTTGGGCAATCCAGATACGCGCAATTCACAAATCAGC 1628
 DB 721 GGCATATATCTCGAATCTGCTTGGGCAATCCAGATACGCGCAATTCACAAATCAGC 780

OY 1629 CCTGGCAGACACGAGCA-GGAGGAGAGACAGAGAAAGAAACACAG-CATGAGAAC 1686
 DB 781 CCTGGCAGACACGAGCA-GGAGGAGAGAGAGAGAGAGAAAGAAACCCGCTTGGAGAC 840
 OY 1687 ACAGTAATGAA--TAAACCATTAATATTTTACCCCTCTGTTCT 1730
 DB 841 ACAGTAATGAAATTAACCATTAATATTTTAAACCCCTCTGTTCT 887

RESULT 2

AL567376/c

LOCUS

DEFINITION

AL567376 LTI_FL013_FBRn1 Homo sapiens cDNA clone CS0DF024Y004 3

prime, mRNA sequence.

AL567376

VERSION

AL567376.1 GI:12920672

KEYWORDS

EST.

SOURCE

ORGANISM

Homo sapiens

human.

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

1 (bases 1 to 814)

Li, W.B., Gruber, C., Jesse, J. and Polayes, D.

Full-length cDNA libraries and normalization

Unpublished (2001)

CONTACT: Genoscope

Genoscope - Centre National de Sequencage

Bp 191 91006 EVRY cedex - France

Email: sequef@genoscope.cns.fr. Web : www.genoscope.cns.fr.

Location/Qualifiers

source

1. 814

/organism="Homo sapiens"

/db_xref="taxon:9606"

/clone_image="CS0DF024Y004"

/clone_1db="LTI_FL013_FBRn1"

/dev_stage="pooled tissue from post conception fetuses (20

week, 24 week and 26 week)"

/lab_host="DH10B"

/note="Organ: Fetal brain; Vector: pCMVSPORT 6; 1st strand

cDNA was primed with a NotI-oligo(dT) primer. Five prime

end enriched, double-stranded cDNA was digested with Not I

and cloned into the Not I and Eco RV sites of the

pCMVSPORT 6 vector. Library was constructed by Life

Technologies. Contact : Feng Liang Life Technologies, a

division of Invitrogen 9800 Medical Center Drive Rockville

, Maryland 20850, USA Fax : (1) 301 610 8371 Email :

liang@lifetech.com URL :

http://fulllength.invitrogen.com"

BASE COUNT 161 a 228 c 210 g 205 t 10 others

ORIGIN

Query Match 40.3%; Score 764.8; DB 9; Length 814;
 Best Local Similarity 97.4%; Pred. No. 6.4e-128;
 Matches 788; Conservative 7; Mismatches 12; Indels 2; Gaps 2;

OY 915 AAGTCAACCCCATGCTGTGTGAACCGAGTCAAGGCGAGCTGGCAGAGTCTGCTT 974
 DB 809 AAGTCAACCCCATGCTGTGTGAACCGAGTCAAGGCGAGCTGGCAGAGTCTGCTT 751
 OY 975 AAGTCAACCGAGTGGGCACTGCTTTTGTAAAGCTCCAGTGCATTCAT-CCCTG 1033
 DB 750 AAGTCAACCGAGTGGGCACTGCTTTTGTAAAGCTCCAGTGCATTCATTCATTC 691
 OY 1034 ATGGGGGAGATGTTGAGACTGAGAGTGAAGTGTCTTATAGGCTGGAGGCGCA 1093
 DB 690 ATGGGGGAGATGTTGAGACTGAGAGTGAAGTGTCTTATAGGCTGGAGGCGCA 631
 OY 1094 GTTCCACTCAAGGCTCCCTGCTTGAATTAACCTTCACTGCTCGTAAGCAATCTTC 1153
 DB 630 GTTCCACTCAAGGCTCCCTGCTTGAATTAACCTTCACTGCTCGTAAGCAATCTTC 571
 OY 1154 TGCAGCAAGATTTGGCTGTTTCCGCTGAGTTGGGCTTAGTGAATCGAGATCAATGA 1213
 DB 1154 TGCAGCAAGATTTGGCTGTTTCCGCTGAGTTGGGCTTAGTGAATCGAGATCAATGA 1213

/note="Organ: eye; Vector: pOTB7; Site_1: XhoI; Site_2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH-MGC Library. I"

BASE COUNT 194 a 201 c 248 g 178 t
ORIGIN

Query Match 36.8%; Score 700.8; DB 12; Length 821;
Best Local Similarity 95.5%; Pred. No. 2,1e-116;
Matches 785; Conservative 2; Mismatches 24; Indels 11; Gaps 6;

```

QY 834 GAAGAGCTGGTAAACATTCGATTAATGACGCTGATGATTTGATGATGCT 893
DB 2 GAAGAGCTGGTAAACATTCGATTAATGACGCTGATGATTTGATGATGCT 61
QY 894 TGAAGAGAGAGGTGAGTGAAGTCAACCCCATGCTGTGTAACCGAGTCAAGGCCA 953
DB 62 TGAAGAGAGAGGTGAGTGAAGTCAACCCCATGCTGTGTAACCGAGTCAAGGCCA 121
QY 954 GCGTGGCAGAGTCTGCTTGAAGTCACTGAGTGGGCACTGCTTTTGAAGCCTC 1013
DB 122 GCGTGGCAGAGTCTGCTTGAAGTCACTGAGTGGGCACTGCTTTTGAAGCCTC 181
QY 1014 CAGTGTCCATTCATCCCTGCTGAGGCGATGTTGAGACGTGACAGAGAGTACGCT 1073
DB 182 CAGTGTCCATTCATCCCTGCTGAGGCGATGTTGAGACGTGACAGAGTACGCT 241
QY 1074 TTCTTAAAGCTGGAAGGCCATTCCTCAAGGCTCCCTGCTTGAATCAAACTTCA 1133
DB 242 TTCTTAAAGCTGGAAGGCCATTCCTCAAGGCTCCCTGCTTGAATCAAACTTCA 301
QY 1134 TCGTCTCGAAAACCATTTCTCGCAGCAGATTTGGCTTTGGCCCTGAGTTGGGCTCT 1193
DB 302 TCGTCTCGAAAACCATTTCTCGCAGCAGATTTGGCTTTGGCCCTGAGTTGGGCTCT 361
QY 1194 AGTGAAGTCAAGATCAAA- - -TGACTGGGAGTCAAGTGGGCTGGGCTGCTCT- - -G 1246
DB 362 AGTGAAGTCAAGATCAAA- - -TGACTGGGAGTCAAGTGGGCTGGGCTGCTCT- - -G 421
QY 1247 AAAAGTCTTAAAGAA- -ATCTTCTCAGTTCTCTTTCAGAGAGTGGGCGCGGACGCGA 1305
DB 422 AAAAGTCTTAAAGAA- -ATCTTCTCAGTTCTCTTTCAGAGAGTGGGCGCGGACGCGA 481
QY 1306 AGAGCAACGGGCGCTGCAAAAGGGGCGCTGCTGGTGGATGCGCATATACGCGCA 1365
DB 482 AGAGCAACGGGCGCTGCAAAAGGGGCGCTGCTGGTGGATGCGCATATACGCGCA 541
QY 1366 GGGCGCTTCTGCTGGTGGGCGCTGCAAGAGGCGGCGAGACAGCAACCTGACG- - -A 1424
DB 542 GGGCGCTTCTGCTGGTGGGCGCTGCAAGAGGCGGCGAGACAGCAACCTGACG- - -A 601
QY 1425 ACCGCGCAAACTGCTCGAGAGACCGGTGTAACAGAGCGGGTTGATGACCGAGTGAAG 1484
DB 602 ACCGCGCAAACTGCTCGAGAGACCGGTGTAACAGAGCGGGTTGATGACCGAGTGAAG 661
QY 1485 TAGAAAAACGCTCCGAGAGAGAGAGATGATACGCGCGGAAGTGAAGTCTGCTC 1544
DB 662 TAGAAAAACGCTCCGAGAGAGAGAGATGATACGCGCGGAAGTGAAGTCTGCTC 721
QY 1545 CAGTGTCTGCTGGTGGCGGCGAGCATGATCTCCGAATCTGGTGGGCTTCCAGCAT 1604
DB 722 CAGTGTCTGCTGGTGGCGGCGAGCATGATCTCCGAATCTGGTGGGCTTCCAGCAT 780
QY 1605 ACGGCCAATGTCAACAAATCAGCCCTGGGCAACAGCAGCA 1646
DB 781 ACGGCCAATGTCAACAAATCAGCCCTGGGCAACAGCAGCA 821

```

RESULT 6

B0006545/c 702 bp mRNA linear EST 26-MAR-2002
LOCUS B0006545
UI-H-E11-aza-n-21-0-UI.s1 NCI_CGAP_E11 Homo sapiens cDNA clone
IMAGE:5846228 3', mRNA sequence.

DEFINITION B0006545
B0006545.1 GI:19731445
EST.

ACCESSION B0006545.1
KEYWORDS

VERSION
SOURCE

ORGANISM

human.

human.

human.

human.

human.

human.

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QY 1374 TCGTGTGGCTGCTGACGAGACGGGCGGAGCAGACACCTGACGACCAACCCGCCGA 1433

Query Match 36.8%; Score 698.8; DB 14; Length 702;
Best Local Similarity 99.7%; Pred. No. 5e-116;
Matches 700; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

FEATURES

source

1..702

/organism="Homo sapiens"

/db_xref="taxon:9606"

/clone="IMAGE:5846228"

/clone_lib="NCI_CGAP_E11"

/div_type="Chondrosarcoma"

/dev_stage="Adult"

/lab_host="DH10B (Life Technologies)"

/note="Organ: Left Pelvis; Vector: p773-Pac (Pharmacia)

with a modified polylinker; Site_1: EcoR I; Site_2: Not I;

NCI_CGAP_E11 is a normalized cDNA library containing the

following tissue(s): Chondrosarcoma. The library was

constructed according to Bonaldi, Lennon and Soares,

Genome Research, 6:791-806, 1996. First strand cDNA

synthesis was primed with an oligo-dT primer containing a

Not I site. Double stranded cDNA was ligated to an EcoR I

adaptor, digested with Not I, and cloned directionally

into p773-Pac vector. The oligonucleotide used to prime

the synthesis of first-strand cDNA contains a library tag

sequence that is located between the Not I site and the

(dT)18 tail. The sequence tag for this library is

ACACTTGAC.

TAG_LIB=UI-H-E11

TAG_TISSUE="chondrosarcoma

TAG_SEQ="ACACTTGAC"

BASE COUNT 137 a 200 c 163 g 202 t

ORIGIN

Query Match

36.8%; Score 698.8; DB 14; Length 702;

Best Local Similarity 99.7%; Pred. No. 5e-116;

Matches 700; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1194 AGTGAAGTCAAGATCAAA- - -TGACTGGGAGTCAAGTGGGCTGGGCTGCTCT- - -G 1253

DB 702 AGTGAAGTCAAGATCAAA- - -TGACTGGGAGTCAAGTGGGCTGGGCTGCTCT- - -G 643

QY 1254 CTTAAGAAATCTTCTAGTTCCTCTTTCAGAGAGTGGGCGCGGAGCGCAAGCAAC 1313

DB 642 CTTAAGAAATCTTCTAGTTCCTCTTTCAGAGAGTGGGCGCGGAGCGCAAGCAAC 583

QY 1314 GGGCGCTGCAAAAGCGGCGCTGCTGGTGGATGCGCATGTACGCGAGCGGCTTC 1373

DB 582 GGGCGCTGCAAAAGCGGCGCTGCTGGTGGATGCGCATGTACGCGAGCGGCTTC 523

/clone.lib="RIKEN full-length enriched mouse cDNA library"
/dev_stage="11 days embryo"
1159.1470
/note="BRAIN CDNA, CLONE MNCB-0671
data source:SPFR, source key:Q9J36, evidence:ISS
putative"

CDS

/codon_start=-1
/protein_id="BAB28220.1"
/db_xref="GI:12849130"
/db_xref="MGD:1919835"
/translation="MLOSQAAEHLPEHLPELRLGHVHEEVDHRAVEEERECQED
HCEPVSSTGVMGFCCSHDPSDLIGHPTHEGRHHNOSWQARTGKRRRGEKHENKN
K"

BASE COUNT 366 a 370 c 405 g 349 t
ORIGIN

Query Match 35.8%; Score 678.8; DB 11; Length 1490;
Best Local Similarity 71.1%; Pred. No. 1.6e-112;
Matches 1023; Conservative 2; Mismatches 369; Indels 44; Gaps 8;

311 GGCCTTGGCTGCAAAATCCAGTGTACACAGTGAAGAATTCACAGTGAACAGACTGC 370
64 GGGCTGGCGCTGCAAAATCCAGTGTACACAGTGAAGAATTCACAGTGAACAGACTGC 123
371 TCCCTCCCGGATTCATTTGAATTCAGAGGTGAACGTTCAAGACATGTGTAGAAAGA 430
124 TCATCCCTGATTCATTCGTAATTCACCGTGAACGTTCAAGACATGTGTAGAAAGA 183
431 GTATGAGAGCAAAAGTGGCGGATCATGTACCGCAAGTCTCTGTCATCATCAGCGCTGT 490
184 GTATGAGAGCAAAAGTGGCGGATCATGTACCGCAAGTCTCTGTCATCATCAGCGCTGT 243
491 CTATGCGCTCTGCTGGGTACCACTCTTCTGTCGCCAGGAAACGTAACTCAGATTTC 550
244 CTATGCGCTCTGCTGGGTACCACTCTTCTGTCGCCAGGAAACGTAACTCAGATTTC 303
551 ATCAGCTGCTGCAACACCCCTCTTGTAAAGGGGCAAGGCCCAAGAAAGGGAAGTTCT 610
304 ATCAGCTGCTGCAACACCCCTCTTGTAAAGGGGCAAGGCCCAAGAAAGGGAAGTTCT 363
611 GCGTGGGCTCTGAGGCGGCTCCGACCAACATCTCTCTCAAAATTAAGCCCTCTTC 670
364 GCGTGGGCTCTGAGGCGGCTCCGACCAACATCTCTCTCAAAATTAAGCCCTCTTC 423
671 TCGGCACTGCTGAAGCTGAAGAGATGCCACCCCTCTCTGCAATGTTCTTCCAGCCCT 730
424 TTGGCACTGCTGAAGCTGAAGAGATGCCACCCCTCTCTGCAATGTTCTTCCAGCCCT 483
731 CGGCCCCAACCCCACTCTCTGAGTGAAGTTCGTTGGGTGTCCTTATTTTCGGGTA 790
484 TCGTCTCTACCTTCCC-----GAGTCTCTTGGGTGTCCTTATTTTCGGGTA 533
791 GGGAGGGGAGTCCGTGTCTCTTGTCTCTGCAAAATA-----TGAAGAGCTC 843
534 GACAAAGGAGTCTTTTGTTCCTCTCTCAAGTAAGCAAGATTCGCGTGCACAAATAC 593
844 GGTAAAGCAATTCGAATTAATTCAGCTGTAAGTGAATTTTCA-----GTATTAATTCAG 898
594 TTTTGAAGCTGTAAGCAATTCGAATTTCTGTGTAGTGAAGAAAAAAGCAT 653
899 GAAGAGGTGAGTGAAGTTCACCCCATGTCTGTGAACCGGAGTCAAGCGGAGCTG 958
654 GGAGAGAAAGTCCAGACCTCCCATCTCCATCTGTTAAACACCGGCAAGCTAGCTG 713
959 GGAGAGTCTGCTTGAAGTCACTAGAGTGGGATGTGCTTTTGAAGCTCTCAGTG 1018
714 GAAGAACCAAG-CTTGAAGTCACTAGAGTGGGATGTGCTTTTGAAGCTCTCAGTG 772
1019 TCCATTCCTATCCCTGATGGGGGATAGT-----TTGAGCTGCAAGAGTGAAGT 1067
773 TCCATTCCTATCCCTGATGGGGGATAGT-----TTGAGCTGCAAGAGTGAAGT 1067
1068 GACGTTTCTTGAAGGGCTGAGGGCTGCAAGCTCAAGCTCCCTGCTTGAACATTCAA 1127

833 TTTTGGCTTTGGGGAGGGGAGAGCCAGTTTGGCTCAAGGCTTCTGAACTTCCATTCA 892
1128 ACTTCATGCTCTGTAAGAACCATTCCTGTCAGCAGAAATTTGCTGTTCGCCCTGAGTTG 1187
893 ACTTCCTGCTCTGTAAGAACCATTCCTGTCAGCAGAAATTTGCTGTTCGCCCTGAGTTG 952
1188 GGTCTGTGATCTGTAAGAACCATTCCTGTCAGCAGAAATTTGCTGTTCGCCCTGAGTTG 1244
953 GTCTGTGATCTGTAAGAACCATTCCTGTCAGCAGAAATTTGCTGTTCGCCCTGAGTTG 1012
1245 TGAAGAGTCTTGAAGAACCATTCCTGTCAGCAGAAATTTGCTGTTCGCCCTGAGTTG 1298
1013 TGAAGAGTCTTGAAGAACCATTCCTGTCAGCAGAAATTTGCTGTTCGCCCTGAGTTG 1072
1299 GACCGCAAGAGCAAGCGGCTGTCAGAAAGCGGCGCTGTGCTGTGAGTGCATGT 1358
1073 GCTAGGAAGATGAGGGGCTGCGGCTGAGCTGTGCTGTGCTGTGAGTGAAGAGCGG 1132
1359 ACAGCAGCGCTTCTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCT 1418
1133 GCAGCTGCGCTTCTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCT 1192
1419 ACAGCAGCGCTTCTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCT 1478
1193 CAGAACACCTTCCGGAACCTGCTGAGAGAGACGTTGTAAGAGAGAGGTTGACCAAGAG 1252
1479 CTGAGGTGAGAAACCTTCCGGAACCTGCTGAGAGAGACGTTGTAAGAGAGAGGTTGAC 1538
1253 CTGAGGTGAGAAACCTTCCGGAACCTGCTGAGAGAGACGTTGTAAGAGAGAGGTTGAC 1312
1539 CTGCTCAGTCTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCT 1598
1313 CTGCTCAGTCTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCT 1372
1599 CAGCATACGGCCAAATGTCACACAAATGACCCCTGAGAGACAGAGAGAGAGAGAC 1658
1373 CAGCATACGGCCAAATGTCACACAAATGACCCCTGAGAGAGAGAGAGAGAGAGAGAG 1431
1659 AGAGAAAGAAAGAAACAGCATGAGAACACAGATTAAGATTAAGATTAAGATTAAGAT 1716
1432 AG 1489

RESULT 8
A1936826/c 678 bp mRNA linear EST 08-MAR-2000
LOCUS A1936826
DEFINITION wp69h10.x1 NCI_CGAP_Brn25 Homo sapiens cDNA clone IMAGE:2467075 3,
similar to SW:GP39_HUMAN 043194 putative G PROTEIN-COUPLED RECEPTOR
GPR39. ; mRNA sequence.
ACCESSION A1936826
VERSION A1936826.1 GI:5675696
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 678)
AUTHORS NCI/NINDS-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE National Cancer Institute / National Institute of Neurological
Disorders and Stroke, Brain Tumor Genome Anatomy Project
(CGAP/BRGAP), Tumor Gene Index
unpublished (1998)
CONTACT Robert Strausberg, Ph.D.
Email: c9apbs-r@mail.nih.gov
Tissue Procurement: David N. Louis, M.D., Myrna R. Rosenfeld M.D.,
Ph.D.
COMMENT cDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima
Bonaldi, Ph.D.
cDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:


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QY 1510 GGAGATCATGTACCCCGGAAAGTAGACCTTCAGTCGTGCTTGGGTTGGCCGAG 1569
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Db 304 GGAGATCATGTACCCCGGAAAGTAGACCTTCAGTCGTGCTTGGGTTGGCCGAG 363
QY 1570 CCATGATCCTCCGAAATGCTGGTGGCATCCAGCATACGCCCAATGTCACACATAGCC 1629
    |||||||
Db 364 CCATGATCCTCCGAAATGCTGGTGGCATCCAGCATACGCCCAATGTCACACATAGCC 423
QY 1630 CTGGGACAGACGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1689
    |||||||
Db 424 CTGGGACAGACGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 483
QY 1690 GTAAATGATTAACCATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1749
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Db 484 GTAAATGATTAACCATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 543
QY 1750 TGGTACCAATTTTTCAGTGTGAGCTTACAGCTTCTTTTGGCACAAGAGAGAT 1809
    |||||||
Db 544 TGGTACCAATTTTTCAGTGTGAGCTTACAGCTTCTTTTGGCACAAGAGAGAT 603
QY 1810 TAACACTGTTTCAAAACCCGGGGAGATTGGCTGTGTTAAAGAGAGACATTAATGCTTA 1869
    |||||||
Db 604 TAACACTGTTTCAAAACCCGGGGAGATTGGCTGTGTTAAAGAGAGACATTAATGCTTA 663
QY 1870 GACAGTGTAAAAAAGAAAAA 1891
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Db 664 GACAGTGTAAAAAAGAAAAA 1891
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RESULT 10
BI917149 747 bp mRNA linear EST 16-OCT-2001
DEFINITION 603181571F1 NIH_MGC_121 Homo sapiens cDNA clone IMAGE:5245648 5',
            mRNA sequence.
ACCESSION BI917149
VERSION BI917149.1 GI:16181111
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
            (bases 1 to 747)
REFERENCE NIH-MGC http://mgc.ncl.nih.gov/
            National Institutes of Health, Mammalian Gene Collection (MGC)
            Unpublished (1999)
            Contact: Robert Strausberg, Ph.D.
            Email: cgabbs-remail.nih.gov
            Tissue Procurement: Life Technologies, Inc.
            CDNA Library Preparation: Life Technologies, Inc.
            DNA Sequencing by: Incyte Genomics, Inc.
            Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LNL at:
            http://image.llnl.gov
            Plate: LLM11619 row: n column: 17
            High quality sequence stop: 737.
            Location/Qualifiers
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            /db_xref="taxon:9606"
            /clone="IMAGE:5245648"
            /clone_1ib="NIH_MGC_121"
            /lab_host="DH10B"
            /note="Organ: Brain; Vector: pCMV-SPORT6; Site_1: Not;
            Site_2: Ecorey (destroyed); RNA source anonymous pool of 3
            fetal brains, female age 20 weeks, female age 24 weeks,
            and male age 26 weeks. Library is oligo-dT primed and
            directionally cloned (Ecorey site is destroyed upon
            cloning). Average insert size 1.7 kb, insert size range
            0.7-3.5 kb. Library is normalized and enriched for
            full-length clones and was constructed by C. Gruber
            (Invitrogen). Research Genetics tracking code 017. Note:

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BASE COUNT 140 a 245 c 216 g 146 t
ORIGIN
Query Match 35.0%; Score 664.2; DB 13; Length 747;
Best Local Similarity 98.6%; Pred. No. 8.3e-110;
Matches 691; Conservative 0; Mismatches 8; Indels 2; Gaps 2;

QY 1 GCCAATCTCCGAGGCTGTGCTGCTCCGCGGAGCGGAGCGGAGAGAGAGAGAGAGAGAG 60
    |||||||
Db 47 GCCAATCTCCGAGGCGG-GGTGTCTGGCCCGGAGCGGAGCGGAGAGAGAGAGAGAGAGAG 105
QY 61 CAGCGCGGAGCGCGGAGCGGCGGAGCGGAGCGGAGCGGAGCGGAGCGGAGCGGAGCGG 120
    |||||||
Db 106 CAGCGCGGAGCGCGGAGCGGCGGAGCGGAGCGGAGCGGAGCGGAGCGGAGCGGAGCGG 165
QY 121 AGCTACGACCGTCTGCTCCGCGGAGAGAGCGGCGGAGCGGAGCGGAGCGGAGCGGAGCG 180
    |||||||
Db 166 AGCTACGACCGTCTGCTCCGCGGAGAGAGAGCGGCGGAGCGGAGCGGAGCGGAGCGGAG 225
QY 181 CGCTGCAAGCGGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 240
    |||||||
Db 226 CGCTGCAAGCGGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 285
QY 241 GCCCGGAGCTCCGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 300
    |||||||
Db 286 GCCCGGAGCTCCGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 345
QY 301 CTTCCTTCCAGGCTTTCGCTGCAATTCAGTGTACAGAGTGTAGAGAGAGAGAGAGAGAG 360
    |||||||
Db 346 CTTCCTTCCAGGCTTTCGCTGCAATTCAGTGTACAGAGTGTAGAGAGAGAGAGAGAGAG 405
QY 361 CAACGACTGCTCTCCCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 420
    |||||||
Db 406 CAACGACTGCTCTCCCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 465
QY 421 TCAGAAAGAGAGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 480
    |||||||
Db 466 TCAGAAAGAGAGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 525
QY 481 AGCGGCTGTCTATGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 540
    |||||||
Db 526 AGCGGCTGTCTATGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 585
QY 541 CTCAGTTTGATGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 600
    |||||||
Db 586 CTCAGTTTGATGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 645
QY 601 GGGAGATTCTGCTCGGCGCTCAAGGCGGAGCGGAGCGGAGCGGAGCGGAGCGGAGCGGAG 660
    |||||||
Db 646 GGGAGATTCTGCTCGGCGCTCAAGGCGGAGCGGAGCGGAGCGGAGCGGAGCGGAGCGGAG 705
QY 661 AGCCCTCTTCTGCGGAG-AGTGTGAAGCTGAAGAGAGATGC 700
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Db 706 AGCCCTCTTCTGCGGAGAGCTGTAAGCTGAGAGAGATGC 746
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RESULT 11
BE217170 799 bp mRNA linear EST 26-OCT-2000
DEFINITION 601141674F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3141450 5',
            mRNA sequence.
ACCESSION BE217170
VERSION BE217170.1 GI:9145793
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
            (bases 1 to 799)
REFERENCE NIH-MGC http://mgc.ncl.nih.gov/
            National Institutes of Health, Mammalian Gene Collection (MGC)
            Unpublished (1999)

```


COMMENT

Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: DCTD/DTF
CDNA Library Preparation: Ling Hong/Rubin Laboratory
DNA Sequencing by: Incyte Genomics, Inc.
DNA Sequencing by: Incyte Genomics, Inc.
clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at: image.lnl.gov
Plate: L10M11 row: c column: 19
High quality sequence stop: 721.

FEATURES

source

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/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:3141450"
/clone_11b="NIH_MGC_9"
/tissue_type="adenocarcinoma cell line"
/lab_host="DH10B (phage-resistant)"
/note="Organ: ovary; Vector: pOTB7; Site: 1: XhoI; Site: 2: EcoRI; CDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies)."

BASE COUNT 171 a 225 c 199 g 204 t
ORIGIN

Query Match 34.7%; Score 658.8; DB 10; Length 799;
Best Local Similarity 96.6%; Pred. No. 7.6e-109;
Matches 767; Conservative 2; Mismatches 14; Indels 11; Gaps 9;

494 ATGCGCTGCGCGGATACAGGCTCTCTCTCCAGGAAAGTACATTCATTCATC 553
1 ATGCGCTGCGCGGATACAGGCTCTCTCTCCAGGAAAGTACATTCATTCATC 59
554 ACTGCTGCAACACCCCTTTTAAAGGCGGCAAGGCGCAAGGGAAGTTCTGCC 613
60 ACTGCTGCAACACCCCTTTTAAAGGCGGCAAGGCGCAAGGGAAGTTCTGCC 119
614 TCGGCGCTGAGGCGGCTCCGACACCAATCTGTTCTTCAATTAAGCCTCTCTG 673
120 TCGGCGCTGAGGCGGCTCCGACACCAATCTGTTCTTCAATTAAGCCTCTCTG 178
674 GCACACTGCTGAAGCTGAAGGAGATGCCAC--CCCTCTGATTTCTTCCAGCCCTC 731
179 GCACACTGCTGAAGCTGAAGGAGATGCCACCCGCTCTGATTTCTTCCAGCCCTC 238
732 GCCCCCAACCCCACTCCCTGAGTGAATTTCTTGGGTGCTTTATTTCTGGGTAG 791
239 GCCCCCAACCCCACTCCCTGAGTGAATTTCTTGGGTGCTTTATTTCTGGGTAG 298
792 GAGAGCGGAGTCCGTCTCTTTTGTCTGCAATTAATGAAGAGCTCGTTAAGC 851
299 GAGAGCGGAGTCCGTCTCTTTTGTCTGCAATTAATGAAGAGCTCGTTAAGC 358
852 ATTCTGAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 911
359 ATTCTGAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 418
912 TGAAGTTACCCCACTGCTGTGTAAACGAGTCAAGGCGAGGCTGGAGAGTCTG 971
419 TGAAGTTACCCCACTGCTGTGTAAACGAGTCAAGGCGAGGCTGGAGAGTCTG 478
972 TTAAGAGTCACTGAGTGGGATCTGCTTTTAAAGCTCCAGTGTCTCATTCATCC 1031
479 TTAAGAGTCACTGAGTGGGATCTGCTTTTAAAGCTCCAGTGTCTCATTCATCC 537
1032 TGAATGGGGGATAGTTGAGAGTCAAGAGTGAAGTGAAGTGAAGTGAAGTGAAG 1091
538 TGAATGGGGGATAGTTGAGAGTCAAGAGTGAAGTGAAGTGAAGTGAAGTGAAG 596

1092 CAGTCCCACTCAAGGCTCCCT--CGCTTGACATTCAACTTCATCTCTGAAAAACATT 1150
597 CAGTCCCACTCAAGGCTCCCTCGCTTGACATTCAACTTCATCTCTGAAAAACATT 656
1151 CTTCTCAGCAGAAATTTGCTGTTTGGCGCTGAGTGGGCTTAG--TGACTGGAACATCA 1209
657 CTTCTCAGCAGAAATTTGCTGTTTGGCGCTGAGTGGGCTTAG--TGACTGGAACATCA 716
1210 ATGA--CTGGAGTCTAGAGTGGGCGGCTGCTCTGAAAGTCTTAAGAAATCTTC 1268
717 ATGAGCTGGGACTTAACCTTGGGCTGCTGCT--TCTGAAGTCTTAAGCAATCTTC 774
1269 TCAGTCTCTCTTGC 1282
775 TCAGTCTCTCTTGC 788

RESULT 12

BE385990

676 bp mRNA linear EST 21-JUL-2000

LOCUS

BE385990

60127636P1 NIH_MGC_20 Homo sapiens CDNA clone IMAGE:3617696 5',

DEFINITION

mRNA sequence.

mRNA sequence.

ACCESSION

BE385990

BE385990.1 GI:9331355

VERSION

EST.

human.

KEYWORDS

human.

human.

ORGANISM

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

REFERENCE

1 (bases 1 to 676)

Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

AUTHORS

NIH-MGC

http://mgc.nci.nih.gov/.

TITLE

National Institutes of Health

Unpublished (1999)

JOURNAL

Unpublished (1999)

Unpublished (1999)

COMMENT

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-remail.nih.gov

FEATURES

source

1..676
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:3617696"
/clone_11b="NIH_MGC_20"
/tissue_type="melanotic melanoma"
/lab_host="DH10B (phage-resistant)"
/note="Organ: skin; Vector: pOTB7; Site: 1: XhoI; Site: 2: EcoRI; CDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies)."

BASE COUNT

168 a 172 c 199 g 137 t

ORIGIN

Query Match 34.7%; Score 657.6; DB 10; Length 676;
Best Local Similarity 99.1%; Pred. No. 1.3e-108;
Matches 672; Conservative 0; Mismatches 4; Indels 2; Gaps 1;

1109 TCCTCGCTTGAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1168
1 TCCTCGCTTGAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 60
1169 TGGTTTCGCGCTGAGTGGGCTCTAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 1228
61 TGGTTTCGCGCTGAGTGGGCTCTAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 120

QY 1229 GGGCTCGGCGCTGCTGTGAAGAGTCTTGAAGAAATCTTTCAGTTTCCTTTCAGAGAGA 1288
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 Db 121 GGGCTCGGCGCTGCTGTGAAGAGTCTTGAAGAAATCTTTCAGTTTCCTTTCAGAGAGA 180
 QY 1289 CTGGCGCGGAG 1348
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 Db 181 CTGGCGCGGAG 240
 QY 1349 GTGGGAGTATACAGGAG 1408
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 Db 241 GTGGGAGTATACAGGAG 300
 QY 1409 CAGCAGCTGACAG 1468
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 Db 301 CAGCAGCTGACAG 360
 QY 1469 GATGACCGAG 1528
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 Db 361 GATGACCGAG 420
 QY 1529 GAATGAG 1588
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 Db 421 GAATGAG 480
 QY 1589 GTTGGGAG 1648
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 Db 481 GTTGGGAG 540
 QY 1649 AGGAG 1708
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 Db 541 AGGAG 600
 QY 1709 AATATTTAG 1768
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 Db 601 AATATTTAG 658
 QY 1769 TTGGAGTTGACAGCTTCT 1786
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 Db 659 TTGGAGTTGACAGCTTCT 676

RESULT 13
 B1919074 704 bp mRNA linear EST 16-OCT-2001
 LOCUS B1919074 603180881f1 NIH_MGC_121 Homo sapiens cDNA clone IMAGE:5244956 5',
 DEFINITION mRNA sequence.
 ACCESSION B1919074
 VERSION B1919074.1 GI:16200128
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 NIH-MGC http://mgi.ncl.nih.gov/
 National Institutes of Health, Mammalian Gene Collection (MGC)
 Unpublished (1999)
 Contact: Robert Strausberg, Ph.D.
 Email: cgaab@remail.nih.gov
 Tissue Procurement: Life Technologies, Inc.
 cDNA Library Preparation: Life Technologies, Inc.
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LNL at:
 http://image.llnl.gov
 Plate: L161618 row: a column: 21
 High quality sequence start: 4
 High quality sequence stop: 702.
 Location/Qualifiers
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 /organism="Homo sapiens"

FEATURES
 source

/db_xref="taxon:9606"
 /clone="IMAGE:5244956"
 /clone_lib="NIH_MGC_121"
 /lab_host="DH10B"
 /note="Organ: brain; Vector: pCMV-SPORT6; site_1: NotI;
 site_2: EcoRV (destroyed); RNA source anonymous pool of 3
 fetal brains, female age 20 weeks, female age 24 weeks,
 and male age 26 weeks. Library is oligo-dT primed and
 directionally cloned (EcoRV site is destroyed upon
 cloning). Average insert size 1.7 kb, insert size range
 0.7-3.5 kb. Library is normalized and enriched for
 full-length clones and was constructed by C. Gruber
 (Invitrogen). Research Genetics tracking code 017. Note:
 this is a NIH-MGC Library.
 BASE COUNT 132 a 237 c 204 g 131 t
 ORIGIN

Query Match 34.3%; Score 651.4; DB 13; Length 704;
 Best local similarity 99.7%; Pred. No. 1.7e-107;
 Matches 663; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

QY 1 GCCAATCCGAGAGAGCTGTGCTGCTGCGCCGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 60
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 Db 40 GCCAATCCGAG 98
 QY 61 CAGCGGAG 120
 |||||||
 Db 99 CAGCGGAG 158
 QY 121 AGCTAG 180
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 Db 159 AGCTAG 218
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 Db 279 GCCCGGAG 338
 QY 301 CTGTGCTTCCAG 360
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 Db 339 CTGTGCTTCCAG 398
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 Db 399 CAGCAGCTGCTCTCCCGAG 458
 QY 421 TCAGAGAAG 480
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 Db 459 TCAGAGAAG 518
 QY 481 AGCGGCTGTCTCATGAG 540
 |||||||
 Db 519 AGCGGCTGTCTCATGAG 578
 QY 541 CTCAGTTTCATCAGTGTGTGCAACACCCCTTTTGAAGGGGCCAAGGGCCCAAGAAAG 600
 |||||||
 Db 579 CTCAGTTTCATCAGTGTGTGCAACACCCCTTTTGAAGGGGCCAAGGGCCCAAGAAAG 638
 QY 601 GGGAGTTTGTGCTGCGGAG 660
 |||||||
 Db 639 GGGAGTTTGTGCTGCGGAG 698
 QY 661 AGCCG 665
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 Db 699 AGCCG 703

RESULT 14
 AM149665/c 690 bp mRNA linear EST 03-NOV-1999
 LOCUS AM149665

DEFINITION xfa40h05.x1 NCI_CGAP_Brn50 Homo sapiens cDNA clone IMAGE:2620569.3', similar to SW:GP39_HUMAN 043194 PUTATIVE G PROTEIN-COUPLED RECEPTOR GPR39, mRNA sequence.

ACCESSION AM149665

VERSION AM149665.1 GI:6197561

KEYWORDS EST.

SOURCE human.

ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo. 1 (bases 1 to 690)

AUTHORS NCI/NINDS-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>. National Cancer Institute / National Institute of Neurological Disorders and Stroke, Brain Tumor Genome Anatomy Project

TITLE (CGAP/Brn50), Tumor Gene Index

JOURNAL Unpublished (1998)

COMMENT Contact: Robert Strausberg, Ph.D. Email: cgapbs-remail.nih.gov

Tissue Procurement: Burt Feuerstein, M.D., Mark Israel, M.D. CDNA Library Preparation: M. Bento Soares, Ph.D. CDNA Library Arrayed by: Greg Lennon, Ph.D. DNA Sequencing by: Washington University Genome Sequencing Center

Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: www-bio.llnl.gov/bdrp/image/image.html

Possible reversed clone: similarity on wrong strand

Seq primer: -400p from Gldco

High quality sequence stop: 402.

Location/Qualifiers

1..690

/organism="Homo sapiens"

/db_xref="taxon:9606"

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/tissue_type="medulloblastoma"

/lab_host="DH10B (phage resistant)"

/note="Organ: brain; Vector: p773D-Pac (Pharmacia) with a modified polylinker; 1st strand cDNA was prepared from a medulloblastoma tumor tissue, and was then primed with a Not I - oligo(dT) primer. Double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified p773 vector. This library is normalized. Library constructed by Bento Soares and M. Fatima Bonaldo."

BASE COUNT 142 a 196 c 160 g 191 t 1 others

ORIGIN

Query Match 34.3%; Score 651.2; DB 10; Length 690;

Best Local Similarity 96.5%; Pred. No. 1.9e-107;

Matches 665; Conservative 0; Mismatches 24; Indels 0; Gaps 0;

QY 1200 TCGAGACTCATGACTGGAGCTTACAGTGGGCTCGCTCTGAAAAGTCTTAAG 1259

DB 689 TCGAAATTCATGACTGGAATTAGACTTGGGCTCGCTCTTTCGAAAGGCTTAAG 630

QY 1260 AAAATCTTCTGCTCTCTTCGAGAGCACTGGCGCGGAGCGCAAGAGCAACGGGCGC 1319

DB 629 AANATCTTCTCAAGTCTCTCTCCAGAGACTGGCGCGGAGCGCAAGAGCAACGGGCGC 570

QY 1320 TCGACAAAGCGGGCGCTGTGGTGTGTGAGTGCATGTACGCGAGCGCTTCTGTGG 1379

DB 569 TCGACAAAGCGGGCGCTGTGGTGTGTGAGTGCATGTACGCGAGCGCTTCTGTGG 510

QY 1380 TTGGCGCTGTGACGAGCAGCGGGCGAGCAGACACTGTGACCAACCCCGCAAACTGC 1439

DB 509 TTGGCGCTGTGACGAGCAGCGGGCGAGCAGACACTGTGACCAACCCCGCAAACTGC 450

QY 1440 TCGAGGAGACCGGTGTACGAGGAGCGGGTGTATGACCGAGCTGAGTAAAGAGTCTGC 1499

DB 449 TCGAGGAGACCGGTGTACGAGGAGCGGGTGTATGACCGAGCTGAGTAAAGAGTCTGC 390

QY 1500 GAGAAAGGAGAGATCATGTACGCCCGAAGTAGACCTGCTCAGTCTGCTTGGGT 1559

DB 389 GAGAAAGGAGAGATCATGTACGCCCGAAGTAGAGACTGTCAGCTGCTGGGT 330

QY 1560 TTGGCGCAGCCGATGATCTCTCCGAAATCTGTGGGCTATTCAGATCGCCCATCTACA 1619

DB 329 TTGGCGCAGCCGATGATCTCTCCGAAATCTGTGGGCTATTCAGATCGCCCATCTACA 270

QY 1620 ACAATCAGCCCGGCGAGCAGCAGAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1679

DB 269 ACAATCAGCCCGGCGAGCAGCAGAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 210

QY 1680 TCGAGACACAGTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1739

DB 209 TCGAGACACAGTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 150

QY 1740 GCGCAGGAAGTGTACCAATTTTTCAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1799

DB 149 GCGCAGGAAGTGTACCAATTTTTCAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 90

QY 1800 AGAGAAATTTTACACTGTTTCAACCCGCGGAGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1859

DB 89 AGAGAAATTTTACACTGTTTCAACCCGCGGAGTGTGTGTGTGTGTGTGTGTGTGTGTGT 30

QY 1860 AAATGCTTTAGACAGTGTAAAAA 1888

DB 29 AAATGCTTTAGACAGTGTAAAAA 1

RESULT 15

B1554034 698 bp mRNA linear EST 05-SEP-2001

LOCUS B1554034

DEFINITION 603235426F1 NCI_CGAP_Brn67 Homo sapiens cDNA clone IMAGE:5309527

ACCESSION B1554034

VERSION B1554034.1 GI:15441348

KEYWORDS EST.

SOURCE human.

ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo. 1 (bases 1 to 698)

AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>.

TITLE NIH-MGC Consortium of Health, Mammalian Gene Collection (MGC)

JOURNAL Unpublished (1999)

COMMENT Contact: Robert Strausberg, Ph.D. Email: cgapbs-remail.nih.gov

Tissue Procurement: David N. Louis, M.D. CDNA Library Preparation: Life Technologies, Inc. CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>

Plate: LNA11784 row: d column: 08

High quality sequence stop: 687.

Location/Qualifiers

1..698

/organism="Homo sapiens"

/db_xref="taxon:9606"

/clone_image="5309527"

/clone_lib="NCI_CGAP_Brn67"

/tissue_type="anaplastic oligodendroglioma with 1p/19q loss"

/lab_host="DH10B (T1 phage-resistant)"

/note="Organ: brain; Vector: pCMV-SPORT6; Site 1: NotI; Site 2: SalI; Cloned unidirectionally. Primer: Oligo dT. Average insert size 2.3 kb. Constructed by Life Technologies. Note: this is a NCI-CGAP Library."

BASE COUNT 131 a 231 c 204 g 132 t

ORIGIN

Query Match 34.0%; Score 645; DB 13; Length 698;

Best Local Similarity 98.7%; Pred. No. 2.4e-106;

		Matches	692:	Conservative	0:	Mismatches	5:	Indels	4:	Gaps	4:
QY	2	CCAACTCCGAGAGGCTCTGTGCTCGCCCGGAGCGCGAGAGAGAGACCCGC	61								
Db	1	CCAATCCGAGAGGCC -GCTGCTCGCCCGGAGCGCGAGAGAGAGACCCGC	59								
QY	62	AGCCGGAGAGCCCGAGAGCGGGCGATGACAGGCTCCGAGCGGACCTGCGGCTCTCTAA	121								
Db	60	AGCCGGAGAGCCCGAGAGCGGGCGATGACAGGCTCCGAGCGGACCTGCGGCTCTCTAA	119								
QY	122	GCTACGACCGTCTGCTCGCGCCGACAGCGGGCCCGAGAGAGCTCGGAGAGAGCC	181								
Db	120	GCTACGACCGTCTGCTCGCGCCGACAGCGGGCCCGAGAGAGCTCGGAGAGAGCC	179								
QY	182	GCTGACAGCCGGGAGAGCTCGGCTGCTGCTGCTGATGCGCTTGCCTCGCGG	241								
Db	180	GCTGACAGCCGGGAGAGCTCGGCTGCTGCTGCTGATGCGCTTGCCTCGCGG	239								
QY	242	CCCCGGAGCTCCGGAGAGATGGGTCTAGGCATCGCGCAACTTTTGGGATTTTC	301								
Db	240	CCCCGGAGCTCCGGAGAGATGGGTCTAGGCATCGCGCAACTTTTGGGATTTTC	299								
QY	302	TTGCTTCAGGCTTTGGCGTCAATCCAGTGTACAGTGTGAAGATTCAGCTGAC	361								
Db	300	TTGCTTCAGGCTTTGGCGTCAATCCAGTGTACAGTGTGAAGATTCAGCTGAC	359								
QY	362	AACGACTGCTCTCCCGAGATTTGATTTGATTTGATTTGATTTGATTTGATTTG	421								
Db	360	AACGACTGCTCTCCCGAGATTTGATTTGATTTGATTTGATTTGATTTGATTTG	419								
QY	422	CAGAAA-GAAGTGTGAGCAAGTCCGGGATCATGTACCGCAAGTCTGTGATCATC	480								
Db	420	CAGAAA-GAAGTGTGAGCAAGTCCGGGATCATGTACCGCAAGTCTGTGATCATC	479								
QY	481	AGCGGCTGTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	540								
Db	480	AGCGGCTGTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	539								
QY	541	CTCAGTTTGCATCAGCTGCTGCAACACCCCTTTTGTAAAGGGCCAGGCCAAGAAAAG	600								
Db	540	CTCAGTTTGCATCAGCTGCTGCAACACCCCTTTTGTAAAGGGCCAGGCCAAGAAAAG	599								
QY	601	GGGAGTTTGGCTCGGCGCCGACAGGCTCGGCAACATCTGTTCTCAAAAT	660								
Db	600	GGGAGTTTGGCTCGGCGCCGACAGGCTCGGCAACATCTGTTCTCAAAAT	659								
QY	661	AGCCCTCTTCTCGGACATGCTGAAGTGAAGAGATGCC	701								
Db	660	AG-CTCTCTCTCGG-ACACTGCTGAAGCTGAAGGAATTTGCC	698								

Search completed: November 7, 2002, 15:03:02
Job time : 2553.39 secs

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